GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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SUMMARIES

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ALIGNMENTS

ABN83947 standard; DNA; 11101 ВP

ABN83947;

02-OCT-2002 (first entry)

Human transporter protein encoding genomic DNA

SNP; Human; transporter protein; zinc transporter; pharmacogenomic analysis; diagnosis; drug screening; gene therapy; kidney; testis; heart; placent small intestine; liver; chromosome 1; single nucleotide polymorphism; gene; ds

Homo sapiens

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/product= "transporter protein"
/note= "contains 7 introns" /*tag= b

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The invention relates to an isolated human transporter protein that is crelated to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease or condition mediated by human transporter protein. The proteins also provide a target for diagnosing a disease or predisposition to disease comediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention components of the speed of the invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention components in the kidney, testis, heart, the protein also been found to be expressed in humans in the kidney, testis, heart, the protein and the protein and to be the protein to the protein the protein to the protein that the protein that
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Matches 390;
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17-NOV-2000;
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  ATTTCTTCTATACCAGTACCGTACTCTCCCCACTGGGATTATTTTAAGGCAAAACC--CA
                                                      GTGCATATTCTTCTCAGCAGATAATATAAAACTTCCACAGGGGCTCCAGACACTGGGCTT
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2000US-0249264.
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3045..45393
                                                                                                                                                                                                                         /product= "Serine/threonine
/note= "Contains 6 introns"
replace(941,T)
                                                                                                                                                                                                                                                                Location/Qualifiers 3000..56067
                  replace(9884..9886,AA)
                                              replace(6983,G)
                                                                         /standard_name= "Single nucleotide polymorphism" replace(6598..9599,AAC,ACC)
                                                                                                      replace(5080,A)
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replace(2612,A)
                            /standard_name= "Single
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/standard_name= "Single nucleotide polymorphism"
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intron variation	variation exon	variation variation	variation variation variation	variation variation	variation variation	variation variation variation	variation variation	variation variation	variation variation variation variation
5761 ag 2 45664,C)	/standard_name= "Single nucleotide polymorphism" FT replace(43357,G) /*tag= ae /standard_name= "Single nucleotide polymorphism" FT /standard_name= "Single nucleotide polymorphism" FT /45394.45525 /number= 2 /number= 2 /xxy	polymorphism" polymorphism"	ard_name= "Single nucleotide polymorphism" e(40731,G) z ard_name= "Single nucleotide polymorphism" e(41303,A) aa ard_name= "Single nucleotide polymorphism" e(4130541306, AAT)	replace(2934,C) *tag= w FT /standard_name= "Single nucleotide polymorphism" replace(34480,G) *tag= x /standard_name= "Single nucleotide polymorphism" replace(38812,C) FT FT FT FT FT FT FT FT FT F	"Single nucleotide polymorphism" 9247, TTA) "Single nucleotide polymorphism" "Single nucleotide polymorphism"	/standard_name= "Single nucleotide polymorphism" FT replace(27399,C) /*tag= r /*tag= r /*standard_name= "Single nucleotide polymorphism" FT replace(28088,A) /*tag= s /*standard_name= "Single nucleotide polymorphism" FT replace(28734,A) /*tag= t FT	ard_name= "Single nucleotide polymorphism" e(26604,A) p pard_name= "Single nucleotide polymorphism" e(27255,G)	/*tag= m FT /stadard_name= "Single nucleotide polymorphism" FT replace(21153,T) /*tag= n FT /standard_name= "Single nucleotide polymorphism" FT replace(256524567,CT) FT replace(256524567,CT)	e(12538,T) g
US6340583-B1. 22-JAN-2002.	variation variation	variation exon	variation variation variation	variation variation	intron variation variation	intron variation exon	intron exon	variation exon	exon intron variation
	replace(56825,A) /*tag bc /standard_name= "Single nucleotide polymorphism" replace(58871,A) /*tag bd /standard_name= "Single nucleotide polymorphism"	/standard_name= "Single nucleotide polymorphism" replace(55499,T) /*tag= ba /standard_name= "Single nucleotide polymorphism" 5592356067 /*tag= bb	replace(54712/C) /*tag= ax /standard_name= "Single nucleotide polymorphism" replace(54799/C) /*tag= ay /standard_name= "Single nucleotide polymorphism" replace(54819,A)	nucleotide nucleotide		5113352775 /*tag= ap /number= 5 replace(52267,A) /*tag= aq /standard_name= "Single nucleotide polymorphism" 5277652933 /*tag= ar /number= 6	50330.51076 /*tag= an /number= 4 51077.51132 /*tag= ao /*tag= 5	/standard_name= "Single nucleotide polymorphism" replace(47908,A) /*tag= al /standard_name= "Single nucleotide polymorphism" 5015550329 /*tag= am /*tag= am	"Single nucleotide

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RESULT 4
ABK8346
ID ABK834
AC ABK834
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                      viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; freematoid arthritis; glomerulonephritis; asthma; thrombos
                                                                 Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                         14-AUG-2002
                                                                                                                                                    ABK83459
                                                                                                                                                                              ABK83459 standard;
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              cardiac reperfusion
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                                                                                                                                                                                                                                                                                                                      GAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-224925/28.
)B; ABB09972.
                                                                                                                                                                                                                                                 GAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCCAGATCACGCCACTGCACTCC
                                                                                                                                                                                                                                                                                                                                                                           ATTAGCTTGGCATGGTCGTGGCCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACACCTATCATCT-----CAGCACTTTGGGAGGCCGAGGCAGGCAGATCATGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACCCAGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACTTCCCAGTGTTCTTGGATAAAGACCAAAATCCTTAACTTGGCCAGGCGCGGTGGCT 12085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACAAAAAAAACTTGACTGTGTCACTCTGTGTTGTCTCCTACCTTGTATACTTCCA 12025
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                                                                                            differentially expressed in granulocytic
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                                                                                                                                                                              CDNA; 128978
            injury; renal reperfusion injury;
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syndrome;
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Pred. No. 2.8e-44;
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                           thrombosis;
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                                                                                                                                                                                                                                         Claim 1;
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                                                                                                                                                                                                                                                                                                                         03-OCT-2000; 2000US-237189P
                                                                                                                                                                                                                                                                                                                                     03-OCT-2001;
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                                                                                                                                                                                                                                                     drug toxicity
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                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC
                                                                                                                                                                                                                                          SEQ ID No
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                                                                                                                                                                                                                                                                                                SM,
                                                                                                                                                                                                                                                                                               Yamaga
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                                                                                                                                                                                                                                                                                               Vockley
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CC (GCA) by detecting the level of expression of spene(s) (Gs) identified by CC DNA chip analysis as given in the specification, and comparing CC the expression level to an expression level in an unactivated CC Also included are modulating (M2) GA by contacting GC with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating (GA) or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject, exposure of a cC subject to a pathogen or sterile inflammatory disease, by detecting the clevel of expression of the gene is indicative of inflammation; (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA, M2 is useful for CC inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA, M2 is useful for cesponse in a subject, exposure of a subject to a pathogen or sterile conflammation (especially chronic) in a tissue, an allergic crosponse in a sethina thorespecially chronic) in a tissue, an allergic crosponse in a subject, exposure of a subject to a pathogen or sterile conflammation (especially chronic) in a tissue, an allergic crosponse in a subject, exposure of a subject to a pathogen or sterile conflammation (especially chronic) in a tissue, an allergic crosponse in a subject, exposure of a subject to a pathogen or sterile conflammation (especially chronic) in a Sequence 128978 BP; The invention relates to detecting (M1) granulocyte (GC) ftp.wipo.int/pub/published_pct_sequences 35134 A; 31020 C; 29358 G; 33466 T; 0 (Gs) identified

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72729

1 CCTGCCACCATGCCTGGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTGCCATGTTG 60 CCGGCCCCCATACCCAGCTAATTTTTATATTTTTAGTAGAGATGGGGTTTTGCCATGTTG

Matches Query Match Best Local

Similarity

21.8%;

Score 217.6; Pred. No. 3.6e 0; Mismatches

.6e-44; DB 24; 204;

Indels

13;

Gaps

2

0,

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RESULT 5
AAL05122/c
ID AAL05122 standard; D
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AC AAL05122;
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Human reproductive s
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Human; reproductive s
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Cancer; gene therapy
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OS Homo sapiens.
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PM W0200155320-A2.
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2000US-0189874
2000US-0190076
2000US-0190076
2000US-020515
2000US-0209467
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                                                                                                                                               The present invention provides the protein and coding sequences o number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence enco
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2000US-0179065.

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2000US-0189874.

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2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0218290. 2000US-0220963. 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0224513.

2000US-0215135 2000US-0216647

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20-OCT 2000
20-OCT
          The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or (c) treating or monitoring treatment of the conditions cited in (b), o monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticol osteoporosis or male osteoporosis, osteopenia, osteodystrophy, osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, progression of the progr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of genes and their expression profiles associated with osteoblas differentiation for screening modulators bone formation, for diagnos or treating e.g. osteoporosis, or as markers for the differentiation
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Pred. No. 3.5e-42;
0; Mismatches 217
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RESULT 8
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2000US-0224519

2000US-0225213

2000US-0225266

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2000US-0225268

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2000US-0225275

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2000US-0198974.
2000US-0190076.
2000US-0199123.
2000US-020467.
2000US-0216486.
2000US-0211647.
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2000US-0231413

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2000US-023398

2000US-0233997

2000US-0233997

2000US-0233963

2000US-0233063

2000US-0233063

2000US-0233063

2000US-0233063

2000US-02334274

2000US-0233998

2000US-0233998

2000US-0233998

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                                              GGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTGTACTAAAAATACAAAAATTAGCTTG
            GCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGCAGTT
                                                                                                                                                                                                                                                                                                                 GCCACCATGCCTGGCTAATTTTTCTTATTTTTAGTAGAGACGAGGTTTTGCCCATGTTGACC
                                                                                                                         TGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAACCTCA
                                                                                                                                                   CTGTACAAAAATAAATTAGCGGCTGGGCACAGTGG---
                                                                                                                                                                                                                         GAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGACATATTT
GCACGGTAGTGCACGCCTGTAATCCCAGCTACTCAGGAGGCTAAGGCAGGAGAATCTCTT
                                                                                                TGCCTGTAATCCTAACACTTTGGGAGGTCGAGGGGGGACGGATCATGAAGTCAGGAGTTCG
                                                                                                                                                                           ATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAACCCCAGA
                                                                                                                                                                                                   AGATGGTTCACTTGCGCCCAGGAGTTCCAGATCAGCCTGGGCAACATGGAGAAACTCTGT
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                                                                                                                                                                                                                                                                          GGATTATAGGCGTGAGCCGCCGCACCCAGCCAACATTTTTTAAATACTGAAAAGTAGAGG
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2000US-02513030
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2000US-0249297.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule encoding a reproductive system antigen , treating or ameliorating a medical condition
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; testicular antigen; testes; cancer; metastasis; immune disorde reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder;
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2000US-0216880

2000US-0217496

2000US-0217496

2000US-0218290

2000US-022964

2000US-0224518

2000US-0225214

2000US-0225214

2000US-0225214

2000US-0225266

2000US-0225266

2000US-0225267

2000US-0225276

2000US-0225277

2000US-0225757

2000US-0225758

2000US-0225758

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2000US-0199076.
2000US-0198123.
2000US-0205515.
2000US-0205467.
2000US-0215135.
2000US-0215135.
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05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

> 20000S-0229513. 20000S-0230437.

2000US-0231244. 2000US-0231413.

2000US-0231414.

2000US-0232080 2000US-0232081 2000US-0231968 2000US-0232397 2000US-0232398 2000US-0232399 2000US-0232399

2000US-0232401. 2000US-0233063. 2000US-0233064. 2000US-0233065.

2000US-0234223. 2000US-0234274. 2000US-0234997.

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Best Local
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular canc
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                                                                                                                                                                                                                                                                                                                                                      GGACCAGCCTGGCCAACATGGTGAAACCCTGTCTGTACTAAAAATACAAAAATTAGCTTG
                                                    TGCCTGTAATCCTAACACTTTGGGAGGTCGAGGGGGACGGATCATGAAGTCAGGAGTTCG
                                                                                   TGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAACCTCA
                                                                                                                                                       CTGTACAAAAATAAATTAGCGGCTGGGCACAGTGG-----
                                                                                                                                                                                                      ATTTCTTCTATACCAGTACCGTACTCTCCCCCACTGGGATTATTTTAAGGCAAAACCCAGA
                                                                                                                                                                                                                                                        AGATGGTTCACTTGCGCCCAGGAGTTCCAGATCAGCCTGGGCAACATGGAGAAACTCTGT
                                                                                                                                                                                                                                                                                                       GAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGACATATTT
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2000US-0249300
2000US-0250390
2000US-0251030
2000US-0251130
2000US-02511479
2000US-02511479
2000US-02511856
2000US-02511868
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2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249264.
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Pred. No. 2.6e-42;
0; Mismatches 201
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מת קיקים להתוכים המוכים להתוכים להתוכי

2000US-0235836. 2000US-0236327. 2000US-0236367. 2000US-0236368.

2000US-0235484 2000US-0235834

2000US-0234998

08-SEP-2000
11-SEP-2000
11-SEP-2000
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03-NOV-2000
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2000US - 0236369 2000US - 0236370 2000US - 0236370 2000US - 0237038 2000US - 0237039 2000US - 0237030 2000US - 0241721 2000US - 0241786 2000US - 0241786 2000US - 0241809 2000US - 0241809 2000US - 0241826 2000US - 0244617 2000US - 0246474 2000US - 0246475 2000US - 0246476 2000US - 0246523 2000US - 0246523 2000US - 0246526 2000US - 0246521 2000US - 0246521 2000US - 0246611 2000US - 0249209 2000US - 0249211 2000US - 0249211

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                (GCA), by detecting the level of expression of gene(s) (GS) identified I DNA chip analysis as given in the specification, and comparing the expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of syntession in a sample of the tissue of gene(s) from GS, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3659
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to detecting (M1) granulocyte (GC) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC INC
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an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 122888 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasitic infection, protozoal infection, fungal infection and M5 useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocyte Note: The sequence data for this patent did not form part
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                                  encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of The anti-(II) antibodies and siaso be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID No 745; 753pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -  \\
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                                                                                                                                                                                           CTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATC
                                                                                                                                                                                                                                                                                                                                                                                   TCAGGACCAGCCTGGCCAACATGGTGAAACCCTGTCTGTACTAAAAATAC-AAAAATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAGCACAGAGAGAAAATAATTTGCTTAAGATCATATAGTAGGCCGGGCGTGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGAATAGTTATAGTGTACCCCATTTACCCATCACTCAGTTTCAACAGCTGGTGACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGATTACAGATGTGAGCCACTGTGCCCAGCCATAATGTGCCTTTCATTTGA---TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACGACGACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGTCATGTTG
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 205.8; DB 22; Length Pred. No. 2e-41; O; Mismatches 222; Indels
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 14-AUG-2000

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          14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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19-MAY-2000;
07-JUN-2000;
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14-AUG-2000;
14-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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14 - AUG -
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07-JUL-2000;
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14-SEP-2000;
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14-AUG-2000;
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11-JUL-2000;
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14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2000;
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune; haematopoietic;
                                      2000US-0228924
2000US-0229343
2000US-0229345
2000US-0229345
2000US-0229513
2000US-0230437
2000US-02310438
2000US-0231244
2000US-0231244
2000US-0231244
2000US-0231244
2000US-0231241
2000US-0231241
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2000US-02314968
2000US-023299
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2000US-0225267
2000US-0225268
2000US-0225268
2000US-0225270
2000US-0225757
2000US-0225759
2000US-0225759
2000US-0225759
2000US-0226279
2000US-02268681
2000US-02268681
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2000US-0227182
2000US-0227009
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2000US-0215135.
2000US-0216647.
2000US-0216887.
2000US-0217487.
2000US-0217496.
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0198123.
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2000US-0209467.
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2000US-0220964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune/haematopoietic antigen; cancer;
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21-OCT-2000
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21-SEP-2000
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                                                                                                    17-NOV-2000;
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17-NOV-2000;
                  2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0249265.
2000US-0249297.
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2000US-0241826.
2000US-0244617.
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2000US-0249212.
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2000US-0246609
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CCAGGTGAGGCGGTGGGCCTGTAATCCCAGCTACTCGGGAAGGCTGAGGCAGGAGAATT CTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATC CACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTAAATCACCTCAGGTCAGGAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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08-DEC-2000; 2000US-0251990

11-DEC-2000; 2000US-0254097

05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48908 BP; 14764 A; 10631 C; 10740 G; 12773 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 37150; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for reventing, diagnosing and/or treating cancers and metastage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represent sequences used in the exemplification of the present invention
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               302
                                                                                    242
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
GATGACATTITATCCCTAAATACTTTAGATAAAG--GTGTTCTTTGAAAAAAATCATAAC
                                                                                                                      ATGATTTGGAAGCAAACAGTACTGCAGTCACACTTTGAGTACCAAATGTTCATCCCTGCA 47045
                                                                                                                                                                                           GCCACCACGCCTGGCAAATTTTGTATTTTTAGTAGAGACAGGGTTTCTCCATGTTGGCC
                                              CCATCTCCTCTGTGGGAGTCTGTGAAGAAAGAATACCTGGAGGTGCCAGGCGTGGTGGCT
                                                                                  TTATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAACCCA
                                                                                                                                                          GGGAATAGTTATAGTGTACCCCATTTACCCATCACTCAGTTTCAACAGCTGGTGACATAT
                                                                                                                                                                                                                               GGATTATAGGCGTGAGCCGCCGCACCCAG--CCAACATTTTTAAATACTGAAAAGTAGA
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   2000US-0186350
2000US-018464
2000US-0198123
2000US-0198123
2000US-0198123
2000US-0205515
2000US-0215135
2000US-02116880
2000US-02116880
2000US-02118290
2000US-0218290
2000US-0218290
2000US-0224518
2000US-0224518
2000US-0224518
2000US-02252526
2000US-02252534
2000US-02252526
2000US-02252534
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2000US-02252534
2000US-02252534
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29-SEP-2000

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29-SEP-2000

20-OCT-2000

20-OC
2000US-0229344.
2000US-0229513.
2000US-0229509.
2000US-0229509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breas and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn'disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
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CTGGGATTATAGGCGTGAGCCGCCGCCCACCCAGCCAACATTTTTTAAATACTGAAAAGTAG
                                                                                                                                       CCTGCCACCATGCCTGGCTAATTTTTTAGTTAGTAGAGACGAGGTTTTTGCCATGTTG
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        2000US-0189874.
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2000US-0209467.
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The present invention provides the protein and coding sequences of number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoprotein of the invention.
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Search completed: March 29, 2003, 17:32:37 Job time: 1112.8 secs

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ALIGNMENTS

FEATURES SOUTCE		TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BE897079 LOCUS DEFINITION
http://image.lln1.gov Plate: LiAM9762 row: f column: 10 High quality sequence stop: 584. Location/Qualifiers 1 .967	Tissue Procurement: ATCC/DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 967) NIH-MGC http://mgc.nci.nih.gov/.	mRNA sequence. BE897079 BE897079.1 GI:10362159 EST. human.	BE897079 967 bp mRNA linear EST 20-OCT-2000 601439635F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924489 5',

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/clone=lib="NIH_MGC_72"
/clone=lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 2 kb. Library constructed
Technologies."
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AGAGACAGA-AATGAAACTCTGTCTCAAAAAACAAACAAACAAAAAAAACCACTATACATA 596
                                                                    GGCATGAACCCGGGAGGCGGTGCTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary: Vector: possible; Site_1: XhoI; Site_2
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Stratagene) and Superscript II RT (Life Technologies)." 176 c 170 g 160 t
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/db_xref="taxon:9606"
/clone="IMAGE:3837367"
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61.8%;
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Pred No. 6e-18;
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                                    297 ACCCAGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCAT 356
                                                                                                                                                       255 ATTTAAAATCTCTGTTGCATCTGTCAGTCTCGAATCTCAAAAAATTACCTTTTGACCTGT
                                                                                                                                                                                                                                                    120 GCTGGGATTATAGGCGTGAGCCGCGCGCACCCAGCCAACATTTTTAAATAC---TGAAAA 176
                                                                                                                                                                                                                                                                                                           135 CCCAGGCTGGTGTTGAACTCTTGGCCTCAAGTGATCCTCCCACCTCCAGCCTTCCTGAAGT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Plate: LLAM10153 row: f column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="duodenal adenocarcinoma, cell line" /lab_host="DHIUB (phage=resistant)" /note="organ: small intestine; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." a 170 c 175 g 144 t
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408 TACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGA 467
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                                               AGAGCTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTACTAAAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RKEN), Genomic Sciences Center (SSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Telones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-105K09.R. Pan troglodytes
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R.Site 2 : SacI
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                                                                                                                                                                               /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
145 c 155 g 163 t
                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                           /clone="PTB-105K09.R"
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                AACTCTTGACCTCAGGTGATCCGCCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCG 135
                                                                                        GGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTGCCCATGTTGACCAGGCTGGTCTCG 75
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AACTCGTGGGCTCAAGTCATGTACCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGGTG
                                                                       GGTAATTTTTGTGGTTTCTTGTAGAGGCAGGGTTTCACCATGTTGCCCCAGTCTGGTCTCA 636
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                                                                                                                                              346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone:
AG106956 1 GI:16727474
GSS.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                              Conservative
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/clone_lib="PTB Chimpanzee Male BAC Library"
172 c 165 g 199 t 3 others
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A., Hattori,M.,
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Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                          /clone="PTB-111K02.R"
                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
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PTB-111K02.R,
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Pan troglodytes DNA, clone: PTB-087A17.R,
AG088170
AG088170.1 GI:16639972
                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                           Tel:81-45-503-9111, Fax:81-45-503-510, Clones are derived from the chimpanzee BAC library PTB This BAC end
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                              562
      BAC end sequences of library RPCI unpublished (1997)
Other_GSSs: RPCI-11-354K9.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                  Homo sapiens Chordata; Craniata; Ve Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 523)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
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                                                                                                                                                                         DNA sequence.
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 Medical Center Dr.,
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/clone_lib="PTB Chimpanzee Male BAC
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 Rockville,
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                                                                                                                   Craniata; Vertebrata; Euteleostomi;
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AAATTAGCTGGGCGTGGTGGCGGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAG
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                                                                            Mammalia; Eutheria; Primates; Catarrhini; HC
1 (bases 1 to 449)
Cheung, V.G., Dalrymple, H.L., Narasimhan, S.,
Raap, A.K., Morley, M. and Bruzel, A.
A resource of mapped human bacterial artific
Genome Res. 9 (10), 989-993 (1999)
                                                                                                                                                                                                                                                                                                                          AZ773470 44
UP_524-15C_T7 RPCIll Human
clone 524-15C, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
Contact: Arcaro MA, Morley M, Department of Pediatrics University of Pennsylvania
                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa;
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Class: BAC ends.
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/db_xref="GDB:7635800"
/db_xref="taxon:9606"
/clone="RPCI-11-354K9"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
122 c 110 g 172 t
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204;
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                        Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                      1 (bases 1 to 394)
Bonaldo, M.F., Lennon, G. and Some some some some subtraction:
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Tel: 215 590 2664
Fax: 215 590 3709
Email: mlennox@mail.med.upenn.edu
Plate: 524 row: C column: 15
Seg primer: T7
                                                                                                                                                                       Contact: Soares, MB
                                                                                                                                                                                           97044477
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/note="Vector: pBACe3.6; RPCI11 Human Male
112 c 84 g 154 t 1 others
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                       GGCCCTGCCCCAGACCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217;
                                                                                                      AA229935 390 bp mRNA linear nc51g10.rl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAC similar to contains Alu repetitive element; contains
                                   AA229935.1
EST.
                                                                       AA229935
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The following repetitive elements were found in this cDNA sequence: 9-272, >ALU 273-346, >POLY_A#Simple_repeat
Homo sapiens
                                                                                       repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence: 9-272, >ALU 2
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UT-E-CRI is a normalized cDNA library containing the following tissue(s): eye anterior segment. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AATGCCGAT. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="eye anterior segment"
/dev_stage="adult"
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/clone_lib="UI-E-CR1"
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/db_xref="taxon:9606"
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                                                                                      element ;,
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68.2%;
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                                                                                         mRNA
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.3e-15;
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                                                                                                                             IMAGE: 101171
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                470 CAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGC
                                                                                                                                                                                                                                                                                  209 CAATAATTAGCCAGGCATGGTGGCGGGCACCTGTCATCCCAGCTACTTGGGAGGCTGAGG
                                                                                                                                                                                                                                                                                                  410 CAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCCAGCTACTCAGGAAGCTGAGG
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                                                                                                                                                           AGATCAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACCCCTGTCTCTACTAAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                         BI823844
603039006F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg,
                                BI82384
                                             mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anat
                BI823844.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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h quality sequence stop: 351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1011714"
/clone_lib_"NCI_CGAP_Pr3"
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/lab_host="DH10B"
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              GI:15935394
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78.3%;
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Pred. No. 1.4e-15;
0; Mismatches 52
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Homo
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IMAGE:5179920 5',
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TTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCA
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                                                                                                           TCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCAGATCACGAGGTCAAGAGA
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                                                                                 TCAACCATCCTGGCTAACGGGGTGAAACCCCGTCTCTACTAAAAATACAAAGATTAGC
                                                                                                                                                                                                                                                                                TTAAAGGAAAACAACTAAGAACACTA--CTTAAGAAAGATAAGAGGCCAGGCGAGGTGGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Plate: LLAM11448 row: 1 column: 01
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Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5179920"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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60.9%;
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Primates;
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Pred. No. 1.2e-15;
0; Mismatches 164;
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                                                                                                                                                                                                                                                                                                       388
                                                                                                                                                                                                                                                                                                                                                     347
                                                                                                                                                                                                                                                                                                                                                                         328 AGATAAAGGTGTTCTTTGAAAAAAATCATAACCTCAGGACCAGCCTGGCCAACATGGTGA 38.7
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                                                                                                                                                                                                                                                    CTTGAATCCGGGAAGCAGAGATTGCAG 507
ACAAACAAACAAAAAAA
                                                                                                                                                             CCAGCTACTCAGGAAGCTGAGGCAGGACAATCGCTTGAACCTGGGAGGCAGAGGTTGCAG
                                                                                                                                                                                CCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGCAG
                                                                   TGAGCTGAGATAGCACCACTACACTCCAGCCTGGGGACAGAGTGAGACTCTGTCTCAAAA
                                                                                                             TGAGCTGAGATTGCAGTCGAGCCTGGGCGACAGAGACAGAAATGAAACTCTGTCTCAAAA 567
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Class:
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Clones are available from Research
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ588276 502 bp DNA CITBI-E1-2635H18.TR CITBI-E1 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Other_GSSs: CITBI-E1-2635H18.TF
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Use of BAC End Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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AQ588276.1 GI:5014956
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1 (bases 1 to 502)
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a 115
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/db_xref="taxon:9606"
/clone="2635H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="sperm"
/note="Vector: pBeloBAC11; S:
CalTech Human BAC Library D"
115 c 100 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CITBI-E1"
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75.5%;
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Pred. No. 1.6e-15;
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                   CATAAAAAT
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                                                               GAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTG
                                                                                                                                                                                                                                                                                                                                                   TCAAGAAATCAAGACCATCCTGGCCAACATGGTGAAGCCCTGTCTCTACTAAAAATACAA 196
                                                                                                                                                             GAGAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACC
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Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones availability, please contact Pieter de Jong

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:
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AQ549290.1
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RPCI-11-428K15.TV RPCI-11 Homo
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Fax: 301 838 0208
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/SEX="Male"
/Cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EC
/note="Vector: pBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="RPCI-11-428K15"
/clone_lb="RPCI-11"
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76.7%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 11-300, >ALU (matched compliment) 434-575, >ALU
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: McCray, PB
McCray Lab
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UI-CF-EC1-acj-c-09-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                    145
 Conservative
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                                                                                                                                                                                constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-CF-EC1 is a normalized clnA library containing the
UT-CF-EC1 is a normalized clnA library containing the
                                                                                                                                                                                                                                                                                                                                        following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was
                                                                                                                      and 380-383
                                                                                                                                    TAG_TISSUE=Normal Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-CF-EC1-acj-c-09-0-UI"
/clone_lib="UI-CF-EC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                      TAG_LIB=UI-CF-EC1
                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Adult and Fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Lung"
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172 c 177 o
               15.6%;
57.9%;
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                                                        http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM1071 row: k column:
Plate: -11+v sequence stop: 562.
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                                               Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: CLONETECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 702)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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/lab_host="DHH10B (Tl phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_l: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); Site_1: Sfil (ggccgcttggcc); Site_2: Sfil (ggccattatggcc); Site_1: Sfil (ggccgcttggcc); Site_1: Sfil (ggccattatggcc); Site_1: Sfil (ggccgctgcgcgctgcgcaffafgcCc-3' and 3' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTMGAGGCCGATTATGCGCC-3' and 3' adaptor sequence: 5'-ATTCTMGAGGCCGATCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.6%; Score 156; DB 12; Length 702; 79.2%; Pred. No. 1.4e-15; tive 0; Mismatches 50; Indels
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
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5 AAACCO		σ σ	6		1 CCTGC	atc cal	SSULT 1 S-09-813-817-3 APPLICANT: YAN, Chunhua et a APPLICANT: YAN, Chunhua et a TITLE OF INVENTION: ASCLATED TITLE OF INVENTION: ACID MO TITLE OF INVENTION UNMBER: CURRENT APPLICATION UNMBER: CURRENT FILING DATE: 2001-0 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Window SEQ ID NO 3 LENGTH: 59065 TYPE: DNA ORGANISM: Human ORGANISM: Human		145.6 145.6 145.6 145.6 145.6	146.2 146 145.8	146.8	148.6	150 149.8
AAACCCAGATGAC	ACATATTTATTTCTTCTATACCAGT	GAGGGAAI NAAAAAA	CTGGGATTATAGGCGTGAGCCGCCGCCACCCAGC 	SCTGGTCT	CACCATGO	h Similarity 73; Conserv	817-3 3, Application US/09813817 0. 6340583 INFORMATION: Chunhou et al. WIT YAN, Chunhou et al. FINVENTION: ISOLATED HUMAN K FINVENTION: ACID MOLECULES FINVENTION: THEREOF FERENCE: CL001178 FERENCE: CL001178 APPLICATION UNMEER: US/09/81 FILING DATE: 2001-03-22 OF SEQ ID NOS: 4 E: FastSEQ for Windows Versic O 3 US 59065 DNA SM: Human SM: Human		114. 14. 14. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15	000.	1 7 7	1790	000
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AAATA CACTT	STACC AGACC	ACCCC CACTC	GCACC	CTCA	TCTTA	Score Pred.); Mis		ALI	0.000	8-09-	8-09- 8-09-	80-8	8-09-
ADACCCAGATGACATTTTATCCCTADATACTTTAGATAAAGGTGTTCTTTGAAAAAATC	GTACTCTCCCCACTGG	AAGTAGAGGGAATAGTTATAGTGTACCCCATTTACCCATCAGCTCAGTTTCAACAGCTGGT 	CAGCCAACA TGGCTGGAAGGAGTG	GGTGATCCGCCTGCC	TTTTAGTAGAGACG 	ore 217.6; DB 4; ed. No. 4.5e-48; Mismatches 204;	NASE PROTEINS, NCODING HUMAN ,817	ALIGNMENTS	US-08-943-607-26 US-08-852-807-12 US-08-852-807-1 US-08-724-394A-20 US-08-724-394A-21 US-08-724-394A-22 US-08-724-394A-22 US-09-488-856A-10	167-681-45 076-011-1 943-607-25	943-607-23 242-948-3 341-587-7	849-701-7 943-607-24	729-995-3 852-807-12
TTCTTTGAAAAAAATC 	GACATATTTATTTCTATAGCCAGTACCGTACTCTCCCCCACTGGGATTATTTTAAGGCA	AGTTTCAACAGCTGGT	CTGGGATTATAGGCGTGAGCCGCCGCACCCAGCCAACATTTTTTAAATACTGAA 	ACCAGGCTGGTCTCGAACTCTTGACCTCAGGTGATCCGCCTGCCT	CCIGCCACCATGCCIGGCTAATTTTCTTATTTTAGTAGAGACGAGGTTTTGCCATGTIG	Length 59065; Indels 13; G	NUCLEIC KINASE PROTEINS,		Sequence 26, Sequence 12, Sequence 20, Sequence 21, Sequence 21, Sequence 22, Sequence 10,	Sequence 4 Sequence 1 Sequence 2	Sequence 2: Sequence 3:	Sequence 2	0 0 0
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Best Local Similarity 63.2%;
Matches 373; Conservative
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TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001178DIV
CURRENT APPLICATION NUMBER: US/09/978,197
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/813,817
PRIOR APPLICATION NUMBER: 09/813,817
PRIOR FILING DATE: 2001-03-22
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TYPE: DNA
ORGANISM: Human
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SOFTWARE: FastSEQ for Windows
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Pred. No. 4.5e-48;
0; Mismatches 204;
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SEQ ID NO 3
LENGTH: 70000
TYPE: DNA
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEP
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GCCACCATGCCTGGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTGCCATGTTGACC
                                                                                                                                                                                                             GGACCAGCCTGGCCAACATGGTGAAAACCCTGTCTGTACTAAAAATAC-AAAAATTAGCTT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACAGAGTGAGACTCCGTCTCAAAAAAAACAAACAAAACAGTAACAACAACAAAAAAT
                              ACAGA-AATGAAACTCTGTCTCAAAAACAAACAAACAAAAAAAACCACTATACATAAAAAT 601
                                                                             TGAATCCGGGAAGCAGAGATTGCAGTGAGCTGGAGTCGAGCCTGGGCGACAGAG
                                                                                                                            GGCGTAGTGGTGGGCACCTGTAATACCAGCTACTCTGGAGGCTGAGGCAGGAGAATTGCT
                                                                                                                                            GGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACT 482
                                                                                                                                                                                             AGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                             CGCCTGTAATCCCAGCATTTTGGGAGGCCGAGGTGGGCGAATCACGAGGTCAGGAGTTCA
                                                                                                                                                                                                                                                                                           TGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAACCTCA 363
                                                                                                                                                                                                                                                                                                                             ATCCAGTGCCAACCATAAAAGGTAAC------CAATGCAGGGCGCGGTGGCTCA 50122
                                                                                                                                                                                                                                                                                                                                                                                                              GAATAGTTATAGTGTACCCCATTTACCCATCACTCAGTTTCAACAGCTGGTGACATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATTACAAGCGTGAGCCACCGTGCCCGGCCTGGCTTACTTTTAAACTG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATTATAGGCGTGAGCCGCCGCCACCCAGCCAACATTTTTTAAATACTGAAAAGTAGAGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCCAGATCACGCCACTGCACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGGTGAGATTGCAGTCGAGCCTGGG
                                                            TGAACTCGGTAGGTAGAGGTTGCAGTGAGCTGAGATCACGCCACTGCACTCCAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                          ATTTCTTCTATACCAGTACCGTACTCTCCCCACTGGGATTATTTTAAGGCAAAACCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 197.8; DB 4;
Pred. No. 8.9e-43;
0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 70000;
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 373; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 12394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09488856A Patent No. 6316259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/488,856A CURRENT FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brett P.
APPLICANT: Robert McKay
APPLICANT: Madeline M. I
APPLICANT: Jacqueline W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/REY: CDS
LOCATION: (5864)...(5974)
NAME/REY: CDS
LOCATION: (7902)...(8032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50423 CACAGTTAATGCTGAAAACACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                     4948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                   4830 CCTGCCACCATGCTTGGCTAATTTTTTTTTTTTAGTAGAGACAGGGTTTCACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION: (2438)...(2625)
5068 AAAAAAATTTTTTTTAAGTGGGGTGGCTGGCGGGGGGGCGCTCACGCCTGTAATCCCAGC
                                                                                                                                                                                                  4890 TTAACCAGGATGGTCTCAATCTCCTGACTTC--GTGATCCACCCACCTCAGCCTCCCAAA
                     235 GACATATTTATTTCTAT-----ACCAGTACCGTACTCTCCCCACTGGGATTATTTT
                                                                                                                                                                  118 GTGCTGGGATTATAGGCGTGAGCCGCCGCACCCAGCC---AACATTTTTTAAATACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602
                                                                                                                                                                                                                  58 TTGACCAGGCTGGTCTCGAACTCTTGACCTCAGGTGATCCGCCTCCCCCAAA 117
                                                                                                                                                                                                                                                                                                  1 CCTGCCACCATGCCTGGCTAATTTTCT---TATTTTTAGTAGAGACGAGGTTTTGCCATG
                                                                TATTTTGGAGAAAAAAATCAGAAGGTGCCATTTGGCTTTTACATGTCAGCAATAAGTTGA
                                                                                              AAGTAGAGGGAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGT
                                                                                                                                 GTGCTGGGATTACAGGCGTGAGCCACCACGCCTGGCCCTGGCCTATCCTTTTAAAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (8121)...(8227)
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Jacqueline Wyatt
                                                                                                                                                                                                                                                                                                                                                                                                                      (11713)...(11786)
                                                                                                                                                                                                                                                                                                                                       Conservative
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63.2%;
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                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                   Score 197.2; DB 4;
Pred. No. 6.7e-43;
0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50445
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                                                                                                                                                                                                                                                                                                                                                                     Length 12394;
                                                                                                                                                                                                                                                                                                                                     Indels 14;
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                5067
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                               288
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RESULT 5
US-08-814-095-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7,
                                                                                                                                                                                                                                      TELEFAX: (248) 539-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SOREY, ...
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5368
                                                                                               DESCRIPTION: NO
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5308
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                           FEATURE:
                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                       MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Montgomery, Ilene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5188
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                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529
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 NAME/KEY:
LOCATION:
                                                                    ORGANISM:
                                                                                                                         DESCRIPTION:
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                            LENGTH:
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RY: U.S.
                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                     linear
promoter
4089..22464
                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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500 No. 6025183thwestern Highway,
                                                                                                                                                                                                                                                                    (248) 539-5050
                                                                                                                            promotor,
                                                                                                                                                                                  double
                                                                                                                                                                                                                                                    539-5055
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IDENTIFICATION METHOD:
OTHER INFORMATION: /fun
OTHER INFORMATION: /evi
OTHER INFORMATION: /evi
OTHER INFORMATION: /gen
OTHER INFORMATION: /num
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
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OTHER INFORMATION: /nun
FEATURE:
                                                                                                                                              FEATURE:
NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
THEORMATION: /number= 2
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NAME/KEY:
LOCATION:
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NAME/KEY:
                                                              NAME/KEY: exon
LOCATION: complement (33779...33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
FEATURE:
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NAME/KEY:
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LOCATION:
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LOCATION:
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 NAME/KEY:
LOCATION:
OTHER INFOF
                                                                                                                                                                                                                                     NAME/KEY: exon

NAME/KEY: exon

LOCATION: complement (34528..34895)

OTHER INFORMATION: /function= "arsenite resistance

OTHER INFORMATION: gene"

OTHER INFORMATION: /gene= "AR"

OTHER INFORMATION: /number= 1
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OTHER INFORMATION:
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OTHER INFORMATION: /ev
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LOCATION:
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OTHER INFORMATION: /ev
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LOCATION: 27005..27274
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ION: complement (33493..33591)
INFORMATION: /gene= "AR"
INFORMATION: /number= 4
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27255..28007
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27385..27387
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28129..28131
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 5
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 4
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/standard_name= "ACHE Promotor"
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 6
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 3
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/gene= "ACHE"
/number= 2
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/gene= "ACHE"
/number= 1
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OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /gene= "ARS"
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LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
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FEATURE:
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
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LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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Local Similarity 61.9%;
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Pred. No. 9.9e-43; 
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Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/345,81 CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                          NAME/KEY: allele
LOCATION: 88073
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ORGANISM: Homo sapiens
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  NAME/KEY: allele
                       LOCATION: 93714
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NAME/KEY: allele
NAME/KEY: 146345
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NAME/KEY: allele
NAME/KEY: 160031
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                                            NAME/KEY: allele LOCATION: 72771.
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LOCATION: 134374
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LOCATION: 108308
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LOCATION: 108149
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LOCATION: 103806
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LOCATION:
                                             OTHER INFORMATION:
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LOCATION: 99094..99140
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OTHER INFORMATION: complement
                                                                                              OTHER INFORMATION:
                                                                                                                                FEATURE:
                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 99094..99140
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                                                                                                                                                                                                                                                                                   LOCATION: 99075..99121
OTHER INFORMATION: polymorphic
                                                                                                                                                                                                                                                                                                                                  LOCATION: 99075..99121
OTHER INFORMATION: polymorphic
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele LOCATION: 99075.
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OTHER INFORMATION: polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele LOCATION: 97130.
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OTHER INFORMATION: polymorphic
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LOCATION: 97130..97177
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LOCATION: 93690..93736
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LOCATION: 90819.
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OTHER INFORMATION: polymorphic
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OTHER INFORMATION: polymorphic
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LOCATION: 88050..88096
                        NAME/KEY:
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LOCATION: 97099.
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KEY: allele
TION: 106918..1
NIFORMATION:
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                                                                                                                              RESULT
                                                                    Sequence 7, Application Patent No. 6025183 GENERAL INFORMATION:
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Best Local
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APPLICANT: Soreq, He APPLICANT: Zakut, HE APPLICANT: Shani, ME TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86354
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OTHER INFORMATION:
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LOCATION: 108127..108177
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LOCATION: 108127..108177
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NAME/KEY: allele
LOCATION: 108084..108130
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LOCATION: 108084
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Pred. No. 1.6e-40;
""amatches 217;
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TRANSGENIC ANIMAL AS
ANTI-CHOLINESTERASE

SUBSTNACES

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TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including
DESCRIPTION: promotor, ACHE gene and AF
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REGISTRATION NUMBER: 23(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                FEATURE:
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OTHER INFORMATION: 24116
OTHER INFORMATION: 24116
OTHER INFORMATION: /evic
OTHER INFORMATION: /gen
OTHER INFORMATION: /numl
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
                                                                         NAME/KEY:
LOCATION:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /ev
OTHER INFORMATION: /ge
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OTHER INFORMATION: /fur
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OTHER INFORMATION: /nur
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LOCATION: 2246
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                          NAME/KEY:
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LOCATION: 24090..25177
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                                                        IDENTIFICATION METHOD:
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25524..26009
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27005..27274
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/standard_name= "ACHE Promotor"
                                                                                                                            OD: experimental
/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                /function= "non-translated"
/gene= "ACHE"
/number= 1
                                                                                                                                                                                                                                                             /evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 2
                                                                                                                                                                                                                                                                                                                       DD: experimental
/function= "(translation start:
24110)"
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DD: experimental
/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 4
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LOCATION: complement
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LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
                                                                                                                                                                                                                                                    LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
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OTHER INFORMATION:
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
                                                                               LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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LOCATION: 28008..2812
IDENTIFICATION METHOD:
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NMATION: /function= "arsenite resistance"
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/gene= "ACHE"
/number= 5
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complement (31131..31284)

/gene= "AR"

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Best Local Similarity
Matches 373; Conserv
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OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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OTHER INFORMATION: /gene= "AR"
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TGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGGTGCAGTGAGCGGAAATCATGCC
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FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                          LOCATION: FEATURE:
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LENGTH: 17327 base pai
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-JUL-1988 ATTORNEY/AGENT INFORMATION: NAME: Cimbala, Michele A
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/224,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                 FEATURE:
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                                                                                      NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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OTHER INFORMATION:

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RESULT 9
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 639373
; Patent No. 639373
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BOUGUELETC, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                                                      SOFTWARE:
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Best Local Similarity
Matches 339; Conserv
                                                                                                                    PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30
                                           ORGANISM: Homo sapiens
                                                            TYPE: DNA
NAME/KEY: allele LOCATION: 72794
                              FEATURE:
                                                                          LENGTH: 162450
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FEATURE:
NAME/KEY: allele
NAME/TON: 99117
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NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION:
 NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION:
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LOCATION: 134374
OTHER INFORMATION:
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LOCATION: 134134
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 99098
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LOCATION: 97122
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LOCATION: 90842
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LOCATION: 108149
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LOCATION: 108106
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NAME/KEY: allele
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LOCATION: 103806
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LOCATION: 93714
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NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: !
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NAME/KEY: allele
NAME/TON: 97099..97145
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NAME/KEY: allele
NAME/KEY: 93690..93736
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LOCATION: 72771..7:
OTHER INFORMATION:
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LOCATION: 160031
OTHER INFORMATION:
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LOCATION: 97130..97177
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OTHER INFORMATION:
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OTHER INFORMATION: polymorphic
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LOCATION: 97099..9;
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LOCATION: 90819..90865
OTHER INFORMATION: com
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic
                                              OTHER INFORMATION:
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OTHER INFORMATION: polymorphic
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LOCATION: 88050..88096
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LOCATION: 72771..72817
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Best Local Similarity 62.9
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NAME/KEY: allele
'TYON: 106918...
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FEATURE:
NAME/KEY: allele
108084..108130
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LOCATION: 103783..103828
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LOCATION: 103783...
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LOCATION: 108127..108177
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LOCATION: 108084..
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GGAGGCTGAGGCAGGAGAATTGCCTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGATAT
                                                                              TACTAJAAATACAJAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCA 458
                                                                                                                      TGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAAATGGTGAAACCTCGTCTC
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N: polymorphic fragment 5-135-198 SEQ ID60
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; LENGTH: 16389
; TYPE: DNA
; ORGANISM: Human
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Best Local :
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CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.9e-38;
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; ORGANISM: Human
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Best Local Similarity
Matches 359; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 3
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEI TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOO1178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
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                                                                                                          TCGAGACTAGCTTGGCCAACATGGCAAAACCCCCATCTCTACTAAAAATTATAAAAATTAGC
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              CTTAAACCCGGGAGGCAGAAGTTGCAGTGAGCCGAAATTGTGCCACTGCACCTTT
                                                                       CTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTGGGCGACAG
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ACCTGTAATCCCAGCACTTTGGGAAGGCCGAGGCAGGTGGA--TCACTTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                   ACACTGGGAAGTTGTGGAAGTATACAAGGTAGGAGAGACAACACAGAGTGACACAGTCAA
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Pred. No. 1.1
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1.1e-36;
hes 227;
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RESULT 12 US-09-978-197-3/c ; Sequence 3, Application

US/09978197

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RESULT 13
US-09-268-992-7/c
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 ; GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Freimer, H.
APPLICANT: FREIMER, H.
TITLE OF INVENTION: I
                                                                                     Sequence 7, Application US/09268992 Patent No. 6342351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6403353
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001178DIV
CURRENT APPLICATION NUMBER: US/09/978,197
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/813,817
PRIOR FILING DATE: 2001-03-22
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ORGANISM: Human
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                                                                                                                                                                                             TTGGCATGGTCGTGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCA 480
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METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING CHROMOSOME-18p RELATED DISORDERS
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60.4%;
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Pred. No. 1.1e-36;
0; Mismatches 227
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FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1998-00-8
EARLIER FILING DATE: 1998-00-8
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER APPLICATION NUMBER: 60/078,044
EARLIER APPLICATION NUMBER: 60/078,044
EARLIER FILING DATE: 1998-03-16
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ORGANISM: Homo
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                                                                                                                                               TCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGC
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                                                             AGTAAGCCAAGATGGCACCACTGCCCCTCTAGCCAGGGCAAAAGAGCCCAGACCCTGTCTCA
                                                                                             AGTGAGCTGAGATTGCAGTCGAGCCTGGGCGACAGAG-ACAGAAATGAAACTCTGTCTCA
                                                                                                                                TCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGTGGAGGCTGC
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US-09-657-474-7/c

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; NAME/KEY: modified_base; LOCATION: all n positions; OTHER INFORMATION: n=a, c, US-09-657-474-7
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CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/268,992
PRIOR FILING DATE: 1999-03-16
PRIOR PPLICATION NUMBER: 09/236,134
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/106,056
PRIOR APPLICATION NUMBER: 60/06,056
PRIOR PILING DATE: 1998-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/088,312
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR FILING DATE: 1998-03-16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: AND TREATING CHROMOSOME-18p FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, H. APPLICANT: Freimer, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44895 AGGGATAACAGGGGTGAGCCACTGCACCCGGCCCTGGACCATTTCTTATTGCAAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                          44655 TTCACTTTGGGAGGCCAAGGTGTGGATCACCTGAGGTCACCAGCCTGGCCAACATGGT
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                                                                                                                                                                                                                                                                               5 CCACCATGCCTGGCTAATTTTCTT--ATTTTTAGTAGAGACGAGGTTTTGCCATGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGACATAT 241
                  TCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGC
                                                                                                                  GAAACCCTGTCTGTACTAAAAATACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAA 445
                                                                                                                                                                                                    AAGGTGTTCTTTGAAAAAAATCATAACCTCAGG-----ACCAGCCTGGCCAACATGGT
                                                                                                                                                                                                                                         ACAGGATCTGAAATTTCTCCTGGTTTACATTGCCCCACCAATAGCCTAAAAAGGTCAAGTT
                                                                                                                                                                                                                                                                                                                                                        TTATTTCTTCTATACCAGTACCGTACTCT-----CCCCACTGGGATTATTTTAAGGCAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GGGATTATAGGCGTGAGCCGCCGCACCCAGCCAACATTTTTAAATACTGAAAAGTAGA 181
TCCCAGCTACTCAGGAGGCTGAGGCAGGAGATCACTTGAACCCAGGAGGTGGAGGCTGC
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Pred. No. 9.4e-36;
1; Mismatches 192;
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SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28687 CCACCATGCCCCACTAATTTTTTGTATTTTTGGTAGAGATGGGGTTTCACCATGTTTCC
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                                                                           TGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTGGGCGACAGAG
                                                                                                                                       GGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACT
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                           TGAACCCGGGAGGCAGAGGTTGCAGTGAACCGAGATTGTGCCACTGCACTCCAGCCTGGT
                                                                                                                       GGCATGGTGGCATGTGCCTGTAATCCCAGTTACTTGGGAAGCTGAGGCAGGATAATTGCT
                                                                                                                                                                                                            AGGACCAGCCTGGCCAACATGGTGAAAACCCTGTCTGTACTAAAAATACAAAAATTAGCTT
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Pred. No. 3.2e-35;
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Search completed: March 29, 2003, 22:40:54 Job time : 1074.43 secs

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Result
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length
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     Published_Applications_NA: *
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UUS-09-764-847-1416
UUS-09-764-887-459
UUS-09-764-887-455
UUS-09-954-531-180
UUS-09-962-435-292
UUS-09-962-832-119
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Sequence 1416, Ap
Sequence 1598, App
Sequence 415, App
Sequence 456, App
Sequence 292, App
Sequence 292, App
Sequence 119, App
Sequence 61, Appli
Sequence 1, Appli
Sequence 15, Appli
Sequence 15, Appl
Sequence 292, App
Sequence 193, App
Sequence 193, App
Sequence 193, App
Sequence 193, App
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Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1416
SEQ ID NO 1416
LENGTH: 32192
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1416, Application US/10092154 Publication No. US20030054375A1
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US-09-764-877-3851	US-09-764-869-1573	US-09-818-512-3	US-09-764-869-2314	US-09-764-869-2326	US-09-967-013-5	US-09-822-846-257	US-10-091-572-874	US-09-764-869-2140	US-09-764-887-456	US-09-764-887-415	US-09-967-768A-314	US-09-764-847-1403	US-10-092-154-1403	US-09-804-471A-3	US-10-238-709-3	US-09-764-877-3798	US-09-764-877-3798	US-09-764-877-3797	US-09-764-877-3797	US-09-764-855-194	US-10-072-349-194	US-09-764-855-193	US-10-072-349-193	US-09-764-855-194	US-10-072-349-194
	Sequence 1573, Ap	Sequence 3, Appli	Sequence 2314, Ap	Sequence 2326, Ap	Sequence 5, Appli	Sequence 257, App	Sequence 874, App	Sequence 2140, Ap	Sequence 456, App	Sequence 415, App	Sequence 314, App	Sequence 1403, Ap	Sequence 1403, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 3798, Ap	Sequence 3798, Ap	Sequence 3797, Ap	Sequence 3797, Ap	Sequence 194, App	Sequence 194, App	Sequence 193, App	Sequence 193, App	Sequence 194, App	Sequence 194, App

ALIGNMENTS

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Best Local Similarity 61.6%;
Matches 382; Conservative
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26110 GCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCCACCTGCCTCTGCCCCCCCAAAGTG
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                                          241 TTTATTTCTTCTATACCAGTACCGTACTCTCCCCACTGGGATTATTTTAAGGCAAAACCC
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Pred. No. 2.6e-48;
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SEQ ID NO 1416
LENGTH: 32192
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 2003
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
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CTGGGATTATAGGCGTGAGCCGCGCGCACCAGCATTTTTAAATACTGAAAAGTAG
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                                                    TTTATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAACCC
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Pred. No. 2.6e-48;
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SEQ ID NO 1598
LENGTH: 11538
TYPE: DNA
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Best Local Similarity 63.9%;
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEO ID NOS: 2442
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
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GCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTT
                                                 GGACCAGCCTGGCCAACATGGTGAAAACCCTGTCTGTACTAAAAAATTACAAAAATTAGCTTG
                                                                                          CATCTGTAATCCCAGCACTTTGGGAGGCTGGCGGGAGGACCACCTAAGGTCAGGAGTTTG 4707
                                                                                                                                                        CTTCGAGAGGTAGACAATAAAATAGTTTTTAAAAATTTTCAGGGAAGGCACAGTGGCTCA 4647
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                                AGACCAGTCTGACCAACATGGTGGAAAACCTGTCTCTACTAAAAATACAAAAATTAGCTAG
                                                                                                                         GACATTTTATCCC-TAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAACCTCA
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Pred. No. 1.6e-48;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 415
LENGTH: 7703
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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TGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGAT----TGCAGTCGAGCCTGGGCGAC
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Pred. No. 1.7e-48;
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US-09-764-887-456
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 658
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. US20020042096A1 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PAll3
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                                                                              TGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGAT----TGCAGTCGAGCCTGGGCGAC
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                                                               TGAACCCAGGAGGTGGAGGTTGCGGTGAGCTGAGATCAAGCCCCATTGCACTCCAGCCTA
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Matches 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77 CURRENT APPLICATION NUMBER: US/09/954,531 CURRENT FILING DATE: 2002-05-02 PRIOR APPLICATION NUMBER: US/05/0233,133 PRIOR FILING DATE: 2000-09-18
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NUMBER OF SEQ ID NOS: 1392
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PRIOR FILING DATE: 2000-09-20
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APPLICATION NUMBER: US/60/234,567
FILING DATE: 2000-09-22
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AGTCGAGCCTGGGCGACAGAGACAAATGAA-ACTCTGTCTCCAAAAACAAACAAACAAACAAACAAA 580
                                                        AATTGAGGCAGGAGAATCGCTTGAACCCCAGGAGGCAGAGGTTGCAGTGAGCCACAATCGT
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SEQ ID NO 292
LENGTH: 65608
TYPE: DNA
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
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CURRENT FILING DATE: 2001-09-25
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PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
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                                                                                                               ATCACTGGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACACCATCTCTAC
                                                                                                                              TEGTCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGGCAG
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                                                        TAAAAGTACAAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTCGGGA
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Pred. No. 2.6e-47;
0; Mismatches 203
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US-09-962-832-119
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Best Local Similarity
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LENGTH: 65608
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APPLICANT: Ebner, R
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Patent No. US20020110821A1
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PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
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CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                              35772 TAAAAGTACAAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTCGGGA
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                                                                    TAAAAATACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCCAGCTACTCAGGA
                                                                                                             ATCACTGGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACACCATCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/245,070 PRIOR FILING DATE: 2000-11-01 NUMBER OF SEQ ID NOS: 16
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TYPE: DNA
ORGANISM: Homo sapiens
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               CTTGAATCCGGGAAGCAGAGATTGCAGTTGAGAT--TGCAGTCGAGCCTGGGCGAC
                                                                               TTGGCATGGTCGTGGGCACCTGTAATCCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCA 480
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Similarity 63.8%;
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FELDHAUS, ANDREW L.
HALDEMAN, BETTY A.
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SEQ ID NO 61
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific
FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Peijing Jeremy APPLICANT: Page, David C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26067 CCATCATGCCCGGCTAATTTTTGGATTTTTAGTAGAGATGGGGTTTCACCATCTTGGCCA 26126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTATAGGCGTGAGCCGCCGCCAGCCAACATTTTTAAATA-----CTGAAAAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTTGAGCTGA 515
                                                                                                                                                              TTCTACTAAAAATACAAAAATTAGCTGGGTGTGATGGCACATGCCTGTAGTCCTAGCTAC
                                                                                                                                                                                     CTGTACTAAAAATTACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTAC
                                                                                                                                                                                                                                             GAGGGTGGATCACAAGATCAGGAGATCGAGACCAGCCTGACCAATATGGTGAAACCCTGT
                                                                                                                                                                                                                                                                                                                          AAACTCTAAGGCCGGGTGTGGTGGCTCACGCCTGTAATTCCAGCACTTTGGGAGGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTACAGGCGTGAGCCACTGCGACCGGCCTAGAAGTTTTTATAAAATATCTTTGCAACA 2624
TCTGGAGACTGAGACAGGAGATCACTTGAATCTGGGAGGCAGAGGTTGCAGTGAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGGTCTTGAACTCCTGATCTCA--TGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGG
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Pred. No. 5.2e-45;
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; ORGANISM: human
US-09-933-267A-1
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US-09-933-267A-1/c
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Best Local Similarity
Matches 373; Conserv
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SEQ ID NO 1
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APPLICANT: Kalush, Francis et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09933267A Patent No. US20020123095A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119089 GGCTGGTCTTGAACTCCTGACCTCAAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGG
                                         118729 CTGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACGCGCCTGTAATCCCAG
                                                                                                                                                                                                                                                                                                118909 AATATTGGAAATAGAGCATTGGACAAAACAAAGAAGTCTACCCTCATAGCAGCTTATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 09/692414
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/768184
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                                                                                                                             118789 CAGCACTTTGGGAAGCCAAGGTCAGGAGTTGGAGACCAGCCCGACCAACGTGATGAAACC
                                                                                                                                                                                                                                                                                                                                                                                    118969 GTTACTCTCAATTTATTCAAAAACTATAATTGACAGTACCCTACCGGCCAGTACGGTTATA 118910
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PRIOR APPLICATION NUMBER: 09/804076
PRIOR FILING DATE: 2001-03-13
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                                                                                                                                                                                                               118849 CTAGTGTAGAGAGACAGACAAATAAATAGGTAGCATACACAGGAGGTTAGAAAGTAATAC 118790
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452 CTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CCACCATGCCTGGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTTGCCATGTTGACCA 64
                                                                  CTGTCTGTACTAAAAATACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAG
                                                                                                                                                                     AAAGGTGTTCTTTGAAAAAAATCATAACCTCAGGACCAGCCTGGCCAACATGGTGAAACC
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-016-725-15
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Best Local Similarity
Matches 372; Conserv
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Patent No. US20020151018A1
GENERAL INFORMATION:
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APPLICANT: Zhang, Lin
APPLICANT: Stenn, Kurt
TITLE OF INVENTION: Stearyl-CoA Desaturase
FILE REFERENCE: J&J22065
CURRENT APPLICATION NUMBER: US/10/016,725
CURRENT FILING DATE: 2002-06-10
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                                                                                                                                                                         1661 TTTGAGACCAGCTTGGCCAACAAAGTGAAATCCCATCTCTACTAAAAATACAAAATCAG
                                                                                                                                                                                                                                             1716 GGGGCCCTACCTCAGCAAAAGGAACAATAGTTACAACAATTATGACAGCAAA----AAG
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                                                                                                                     420 CTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 GGGATTATAGGCGTGAGCCGCACCCAGCC ---AACATTTTTTAAATACTGAAAAGTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                      180 GAGGGAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGACAT 239
540 GAGACAGAAATGAA-ACTCTGTCTCAAAAACAAACAAACAA 579
                                                                                                                                                                                                                                                                              300 CAGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAAC
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                                                     ACTTGAATCCGGGAAGCAGAGATTGCAGTGAGGTGAGATTGCAGTCGAGCCTGGGCGACA
                                                                                                      CTGGGCATGGTGGGAAGTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATT
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Pred. No. 3.9e-45;
0; Mismatches 191; Indels 18;
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US-09-954-531-180/c
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PRIOR FILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR APPLICATION NUMBER: US/60/234,567
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SEQ ID NO 180
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Best Local Similarity
Matches 377; Conserv
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CURRENT FILING DATE: 2002-05-02
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LOCATION: (1)...(65608)
OTHER INFORMATION: n=a,t,g
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                   CCTCAGGACCAGCCTGGCCAACATGGTGAAAACCCTGTCCTGTACTAAAAATTACAAAAATTA 418
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                                                                                                                                                            GCTCACGCCTGTAATCCCAACACTTTGGGAGGTCAGAGTGGTTGGATCACGAGGTCAGGA
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APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/962,436

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US/60/235,082

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/234,924

PRIOR FILING DATE: 2000-09-25
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ORGANISM: Homo
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                                                   GTTTGAGACCAGCCTGACCAACATGGTGAAAACCCTGTCTCTACTAAAAACGCAAAAATTA
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Pred. No. 2.6e-44;
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US-09-962-832-119/c
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Best Local Similarity
Matches 377; Conserv
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// Cgn 2_6/ptodata/1/pna/US6024_COMB. seq:
// Cgn 2_6/ptodata/1/pna/US6025_COMB. seq:
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// Cgn 2_6/ptodata/1/pna/US6025_COMB. seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 62, Appl	Sequence 6, Appli	Sequence 4301, Ap	Sequence 6, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 11622, A	Sequence 9471, Ap	Sequence 780, App	Sequence 24569, A	Sequence 24569, A	Sequence 24569, A	Sequence 39, Appl	Sequence 131, App	Sequence 7828, Ap	Sequence 18017, A	Sequence 18017, A	Sequence 18017, A	Sequence 19572, A	Sequence 19572, A	Sequence 19572, A	Description	

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APPLICANT: Drmanac, Radoje T.

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT APPLICATION NUMBER: 60/125,453
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR APPLICATION NUMBER: 1699-03-19
INUMBER OF SEQ ID NOS: 116231
SOPTWARE: Hy-Patent.pl Version 3.1
SEQ ID NO 19572
LENGTH: 438
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-528-409-19572/c
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                                                                                                               TGGTCTGATGCAGGGACCTGTAACCTGCGTTGTAACACCTTCTCCAGGTAATGCTGAGCC
                                                                                                                                                                          CCCCAGACCTACTGAATCCTGGAAATATTCAGGCTCCACACCCCAGAGATTCTGGTTCGGT
                                        TGCTGGTGCTCAGAGTAGACAGACCTGGAGAAAACCAGGGTGTCTGAGGTTTTCCAGAAG
                                                                                                                                                            CCCCAGACCTACTGAATCCTGGAAATATTCAGGCTCCACACCCCAGAGATTCTGGTTCGGT
                                                                                                                                                                                                                      ATGAACAATGATGCCACAATAGCACCAGAGAATTTTATAAATACAGATTCCCCAGGCCCTG
                                                                                                 TGGTCTGATGCAGGGACCTGTAACCTGCGTTGTAACACCTTCTCCAGGTAATGCTGAGCC
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4 US-60-226-176-1562

6 US-60-233-468-1562

7 US-60-233-468-1562

5 US-60-233-468-1562

6 US-60-233-468-1162

6 US-60-243-468-9

8 US-60-243-468-9

9 US-60-243-468-9

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RESULT 3
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-933-524-19572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Wovel Nucleic Acid Seque
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-03-17
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SOFTWARE: Hy-patent.pl Version
SEQ ID NO 19572
LENGTH: 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%;
Local Similarity 99.0%;
les 397; Conserva+
                                                                                                                                                                                                                                                                                                                                      CCTCACATCCTCACTGCCACCCCGTCTCCTACAAGATGAGAGACCTGAAAGAGCCCCT 959
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TCCTGTCCCCAGTGGTGTGGGCCAAGAGGCCTGCACCTCTGA 1000
                                                                    CCTCACATCCTCACTCCTGGCACCCCGTCTCCTACAAGATGAGAGACTGAAAGAGCCCCT
                                                                                                                                            AAAACCAGAGTCCAGAGAAGCAGAGAGGCACTCAGTGAGGACCCAAGCAGAGCGGGTGCA 899
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                                                   CCTCACATCCTCACGCCTGGCACCCCGTCTCCTACAAGATGAGAGACTGAAAAGAGCCCCCT
                                                                                                                          AAAACCAGAGTCCAGAGAAGCAGAGAGGCTCTCAGTGAGGACCCAAGCAGAGCGGGTGCA
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Pred. No. 2.8
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APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: NOWBER: US/09/528,409
CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEO ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
                                                                                                                                                                                                                                                                              RESULT 4
US-09-528-409-18017/c
; Sequence 18017, Application US/09528409
; GENERAL INFORMATION:
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APPLICANT: Drmanac, R
APPLICANT: Labat, Iv
APPLICANT: Stache-Cr
APPLICANT: Dickson,
APPLICANT: Jones, Le
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PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEO ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEO ID NO 19572
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Best Local Similarity
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: NOVEL Nucleic Acid Sequences
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
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Pred. No. 2.8e-42;
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                                                                                                               ; ORGANISM: Homo sapiens US-09-933-524-18017
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                                                      Query Match
Best Local Sim
Matches 364;
                                                                                                                                                                    SOFTWARE: Hy-patent.pl Version SEQ ID NO 18017
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Best Local Similarity 84.3%;
Matches 364; Conservative
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APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 116231
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Drmanac,
                                                                                                                                        LENGTH: 449
TYPE: DNA
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447 TTTTGAATAGGAATCATACCGTCAGGACGAGCCCCCCCAAACATGTTTTAACAACGGCCC
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                                                                    Similarity
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                                                      Score 302; DB 35;
Pred. No. 2.9e-30;
0; Mismatches 65;
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Pred. No. 2.9e-30;
0; Mismatches 65;
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US-09-933-524A-18017/c
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PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 18017
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18017, Application US/09933524A GENERAL INFORMATION:
                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 774
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Nucleic Acid Sequences TITLE OF INVENTION: From Various Libraries
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           GTACTAAAAATACAAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTC
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                                                  TAGGCCTTGAGTCTGTAGCGTTCGCTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAG
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 ATTGCAGTCGAGCCTGGAGTACAGAGACAGAAATGAACCTGTGTCTCAAAGACGAGCAAA
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Stache-Crain, Birgit
Dickson, Mark
Jones, Lee W.
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No. 2.
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2.9e-30;
hes 65;
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; NAME/KEY: unsure
; LOCATION: 89-150,
; OTHER INFORMATION:
US-60-182-316-7828
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CURRENT FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 14,630
SOFTWARE: PERL Program
SEQ ID NO 7828
LENGTH: 557
TYPE: DNA
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APPLICANT: Curti; Anne L.
APPLICANT: Lagace, Robert E.
APPLICANT: Klingler, Tod M.
APPLICANT: Stuve, Laura L.
TITLE OF INVENTION: CpG Island Polynucleotides
FILE REFERENCE: PX 0003 P
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OTHER INFORMATION: Inc
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AGCAGAGAGGCACTCAGTGAGGACCCAAGCAGAGCGGGTGCACCTCACATCCTCACTCCT
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Pred. No. 4.1e-26;
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SEQ ID NO 131
LENGTH: 35934
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN I
TITLE OF INVENTION: NUCLEIC ACID MOI
TITLE OF INVENTION: AND USES THEREOI
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Best Local Similarity
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CURRENT FILING DATE: 2000-10-27
NUMBER OF SEO ID NOS: 2121
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                                                      ACTTGAATCCGGGAAGCAGAGATTGCAGTGAGGTGGAGTTGCAGTCGAGCCTGGGCGACA 539
                                                                                                                        CTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATC 479
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 GAGACAGAAATGAA-ACTCTGTCTCAAAAAACAAACAAACAAAAAAAAAC-CACTATACATAA 597
                                    GCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGTTGAGATTGTGACCCTGCACTCCAGTCT
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Pred. No. 1.5e-21;
0; Mismatches 202;
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000609
CURRENT FILLOTION NUMBER: US/60/207,317
CURRENT FILLING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ
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GGCGACAGAGACAGA-AATGAAACTCTGTCTCAAAAACAAACAAACAAAAAAAAACCACTAT 591
                                                                     GAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTG
                                                                                                                            AAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAG
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                                                       GAGGATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATCATACTACTGCACT
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Similarity 65.8%;
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Pred. No. 6.6e-21;
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RESULT 10

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RESULT 11
US-09-764-905-24569/c
US-09-764-905-24569, Application US/09764905
; Sequence 24569, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins,
; FILE REFERENCE: PC004
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CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 42506
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24569
LENGTH: 10702
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CURRENT APPLICATION NUMBER: US/09/764,905
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No. 1.1e-20;
                           and Antibodies
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PRIOR AP PRIOR FILING DATE: PRIOR APPLICATION NUMBER: 60/214,886 PRIOR FILING DATE: 2000-06-28 PRIOR PRIOR PRIOR FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
FILING DATE: 2000-09-25
APPLICATION NUMBER: 60/229,343 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225,267 FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447 FILING DATE: 2000-1; APPLICATION NUMBER: FILING DATE: FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/241,809 FILING DATE: 2000-09
APPLICATION NUMBER: APPLICATION NUMBER: 60/225,757 FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496 APPLICATION NUMBER: 60/220,963 FILING DATE: 2000-02-04 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: APPLICATION APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/244,617 APPLICATION NUMBER: 60/241,785 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/249,299 APPLICATION NUMBER: 60/220,964 FILING DATE: APPLICATION NUMBER: 60/236,369 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/224,518 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/228,924 FILING DATE: 2000-08-30 FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/234,274
FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/234,223
APPLICATION NUMBER: 60/234,223
APPLICATION NUMBER: 60/234,223 FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834 FILING DATE: 2000-08
APPLICATION NUMBER: APPLICATION NUMBER: 60/225,270 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/216,880 FILING DATE: 2000-07-07 FILING DATE: FILING DATE: FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: NT FILING DATE: 2001-01-17 APPLICATION NUMBER: 60/179,065 DATE NUMBER: 60/251,856 2000-08-22 2000-09-01 2000-12-08 2000-09-29 2000-09-29 2000-11-17 2000-08-1 2000-08-14 2000-07-11 2000-12-08 2000-08-14 2000-11-01 2000-07-2000-08-14 2000-08-14 2000-01-3 60/229 60/251,868 60/236,368 60/225 60/236,327 60/224,519 60/251,869 60/218,290 60/225,758 60/217,487 60/180,628

OR FILING DATE: 2000-09-01

OR APPLICATION NUMBER: 60/229,287

OR FILING DATE: 2000-09-01

OR APPLICATION NUMBER: 60/229,513

OR FILING DATE: 2000-09-05

OR PAPPLICATION NUMBER: 60/231,413

OR FILING DATE: 2000-09-08

NUMBER: 60/229,345

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OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,264
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OR APPLICATION NUMBER: 60/232,399
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,401
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/241,808
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,826
OR APPLICATION NUMBER: 60/241,826
OR APPLICATION NUMBER: 60/241,786
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-10-20
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DR FILLING DATE: 2000-09-08
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DR FILLING DATE: 2000-09-08
DR FILLING DATE: 2000-09-08
DR APPLICATION NUMBER: 60/231,414
DR FILLING DATE: 2000-09-08
DR APPLICATION NUMBER: 60/233,064
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Local Similarity 64.4%;
nes 390; Conservative
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RR FILLING DATE: 2000-10-20
DR APPLICATION NUMBER: 60/246,475
RR FILLING DATE: 2000-11-08
DR APPLICATION NUMBER: 60/231,243
DR APPLICATION NUMBER: 60/231,243
DR FILLING DATE: 2000-09-08
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APPLICATION NUMBER: 60/
FILING DATE: 2000-09-14
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FILING DATE: 2000-09-14
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Pred. No. 1.1e-20;
0; Mismatches 205;
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OR APPLICATION NUMBER: 60/249,210
OR FILING DATE: 2000-11-17
OR FILING DATE: 2000-11-17
IOR APPLICATION NUMBER: 60/226,681
IOR APPLICATION NUMBER: 60/226,759

APPLICATION NUMBER: 60/249,216 APPLICATION NUMBER: 60/246,532 APPLICATION NUMBER: FILING DATE: 2000-1

60/241,787

DATE:

FILING DATE:

FILING DATE: APPLICATION NUMBER:

2000-11-08 2000-10-20 2000-10-13

60/246,474

APPLICATION NUMBER: 60/225,213 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/225,759 FILING DATE: 2000-08-14

FILING DATE: APPLICATION NUMBER:

2000-08-22

60/227,182

FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/240,960
FILING DATE: 2000-10-20

FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,040

APPLICATION NUMBER: 60/237,037

2000-10-02

FILING DATE:

APPLICATION NUMBER: 60/ FILING DATE: 2000-10-13

60/239,935

APPLICATION NUMBER: 60/239,937

APPLICATION NUMBER: 60/236,370 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/236,802

APPLICATION NUMBER: 60/237,038 FILING DATE: 2000-10-02

APPLICATION NUMBER: 60/236,367 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/237,039 FILING DATE: 2000-10-02

FILING DATE:

2000-09-05

APPLICATION NUMBER: 60,

/229,509

R APPLICATION NUMBER: 60/225,214

SR FILING DATE: 2000-08-14

SR APPLICATION NUMBER: 60/235,836

SR FILING DATE: 2000-09-27

SR APPLICATION NUMBER: 60/230,438

SR FILING DATE: 2000-09-06

R FILING DATE: R APPLICATION N R FILING DATE:

NUMBER: 60/3: 2000-06-30

60/215,135

APPLICATION NUMBER.
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/249,218
APPLICATION NUMBER: 60/249,218
CONTROL DATE: 2000-11-17

FILING DATE:

2000-11-17

DR APPLICATION NUMBER: 60/249,213
RR FILLING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,212
RR FILLING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,207
DR FILLING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,245
DR APPLICATION NUMBER: 60/249,245
DR APPLICATION NUMBER: 60/249,245
DR APPLICATION NUMBER: 60/249,244
DR APPLICATION NUMBER: 60/249,244
DR APPLICATION NUMBER: 60/249,244

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APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC ACIDS, Proteins, an
FILE REFERENCE: PC004C1
CURRENT APPLICATION NUMBER: US/10/092,399
CURRENT FILING DATE: 2002-03-07
NUMBER OF SED ID NOS: 42506
Prior Application removed - See File Wrapper or
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24569
LENGTH: 10702
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Matches 390
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TYPE: DNA
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                                           GAGAACTAGAAATCATAAAAGAAAAAAATTTAGCGAGCGGATCACCTGAGGTCAGGAGTT
                                                                     GATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCATAACCT
                                                                                                ATTTCTTCTATACCAGTACCGTACTCTCCCCCACTGGGATTATTTTAAGGCAAAACC--CA
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Pred. No. 1.1e-20;
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US-09-973-278-780/c
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CURRENT FILING DATE: 2001-10-10
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APPLICATION NUMBER: 60/051,932
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APPLICATION NUMBER: 60/051,916
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APPLICATION NUMBER: 60/052,803
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APPLICATION NUMBER: 60/051,925
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APPLICATION NUMBER: 60/051,929
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APPLICATION NUMBER: 09/227,357
FILING DATE: 1999-01-08
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APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919
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APPLICATION NUMBER: 60/052,733
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APPLICATION NUMBER: 60/051,926
FILING DATE: 1997-07-08
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                                                                                      APPLICATION NUMBER: 60/055,722
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/051,931 FILING DATE: 1997-07-08
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FILING DATE: APPLICATION I
               APPLICATION NUMBER: 60/055,948 FILING DATE: 1997-08-18
                                               APPLICATION NUMBER: 60/055,723 FILING DATE: 1997-08-18
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                               CTTGAATCCGGGAAGCAGAGTTGCAGTGAGCTGAGAT----TGCAGTCGAGCCTG
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OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: PCT/US00/06049
OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: PCT/US00/06057
OR APPLICATION NUMBER: PCT/US00/06824
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OR FILING DATE: 2000-03-16
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DR FILING DATE: 2000-03-22
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FILING DATE: 2000-03-16
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OR FILING DATE: 2000-04-06
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Query Match 21.8%; Score 217.6; DB 36; Length 1932; Best Local Similarity 63.2%; Pred. No. 1.9e-19; Matches 373; Conservative 0; Mismatches 204; Indels 13; Gaps

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APPLICANT: ROSEN, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper (
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11622
LENGTH: 1932
TYPE: DNA
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Sequence 846, App
Sequence 181, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 25, App
Sequence 73, Appl
Sequence 117, Appl
Sequence 117, Appl
Sequence 2143, Appl
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US-09-691-219-3
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GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al.
APPLICANT: WEI, MING-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1000; DB 6; Best Local Similarity 100.0%; Pred. No. 2.1e-136; Matches 1000; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2000-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                  241 TTTATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAACCC
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NAME/KEY: misc_feature; LOCATION: (1)...(177528); OTHER INFORMATION: n = A US-60-449-629-846
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CANCER, METHODS OF DETECTION AND USE:
FILE REFERENCE: CL001449
  Query Match
Best Local
                                                                                                                     SEQ ID NO 846
                                                                                                                             CURRENT APPLICATION NUMBER: US/60/449,629
CURRENT FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 2712
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)...(630470)
; OTHER INFORMATION: n = A
US-09-947-911-181
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                                Query Match
Best Local S
Matches 421
                                                                                                                                                                                                                                                                                                           Sequence 181, Application US/09947911
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 181
LENGTH: 630470
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                                                                                                                                                                        TYPE: DNA
ORGANISM: HUMAN
FEATURE:
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                              Score 226.6; DB 5;
Pred. No. 2e-25;
D; Mismatches 209;
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US-60-446-133-345/c
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Sequence 345, Application US/60446133
GENERAL INFORMATION:
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                                                                                                                                                                                       TITLE OF INVENTION: Method for Monitoring Anti-Cancer Drug Activities FILE REFERENCE: AMIO1055-2 CURRENT APPLICATION NUMBER: US/60/446,133 CURRENT FILING DATE: 2003-02-11 NUMBER OF SEQ ID NOS: 386 SOFTWARE: Patentin version 3.1 SEQ ID NO 345 LENGTH: 128978
                                                                                                       Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                APPLICANT: Twine, Natalie E
APPLICANT: Dorner, Andrew E
APPLICANT: Trepicchio, William E
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wyeth
                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99443 AAACCT-----TCTCTAAGCACCCTGCATAGAACCACATTTTAGAGGCCCAGGCGTGGTG
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                                                                    Local Similarity
mes 373; Conser
                   1 CCTGCCACCATGCCTGGCTAATTTTTCTTATTTTTAGTAGAGACGAGGTTTTTGCCATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGACAGAAATGAA-ACTCTGTCTCAAAAAACAAACAAACAAAAAAAAC-CACTATACATAA
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CCGGCCCCCATACCCAGCTAATTTTTATATTTTTAGTAGAGATGGGGTTTTTGCCATGTTG 72670
                                                                                                                                                                                                                                                                                                                                                                                   Burczynski, Michael E
                                                                    Conservative
                                                                                   21.8%;
63.2%;
                                                                    0;
                                                                 Score 217.6; DB 9;
Pred. No. 6e-24;
0; Mismatches 204;
                                                                                                   Length 128978;
                                                                    Indels
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nicholas M. Dean
APPLICANT: C. Frank Bennett
APPLICANT: Kennett W. Dobie
TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
FILE REFERENCE: PTS-0043
                                                                                                                                                           122866 CCTGCCACCATGCCAGGCTAATTTTTGTATTTTAGTAGAGACGGGGTTTCTCCATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/304,019 CURRENT FILING DATE: 2002-11-23
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 147
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: H. sapiens
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                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                     LENGTH: 126974
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   AGGGAATAGTTATAGTGTACCCCA - - - - - - - TTTACCCATCACTCAGTTTCAACAGCTG
                                 CTGGGATTACAGGCATGAGCCACGGCGCCTGGCTGCATATGTGTTCTTATTAAACCATAA 122687
                                                              CTGGGATTATAGGCGTGAGCCGCCGCCCCCAGCCAACATTTTTAAATACTGAAAAGTAG
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                                                                                                                                                                                                                         Score 211.8; DB 8; Pred. No. 4.1e-23; 0; Mismatches 207;
                                                                                                                                                                                                                                                      Length 126974;
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RESULT 6
US-60-427-982-322/c
Sequence 322, Application US/60427982
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-60-427-982-322
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 322
LENGTH: 170245
TYPE: DNA
                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/427,982
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dorner, Andrew APPLICANT: Trepicchio, William TITLE OF INVENTION: METHODS FOR DIAGNOSING FILE REFERENCE: AM101055
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                                                                                                                       TCAGGCTGGTCTTGAACTCCTGACCTCAGGTTATCTGCCCGCCTCAGCCTCCCAAAGTGT
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TAAGAAATGCCTGGAACTTCTAAGAAAAAAAAAAAAACCTGAATGAGTTAAAAATTAGAC
                         TAGAGGGAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGAC
                                                   GCAAAACCCCAGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAA 351
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                                                                                                                                                                                                                 al Similarity 61.4
374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Twine, Natalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burczynski, Michael
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                                                                                                                                                                                                                             21.0%;
61.4%;
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                                                                                                                                                                                                                 0;
                                                                                                                                                                                                               Score 210.2; DB 9;
Pred. No. 6.5e-23;
0; Mismatches 228;
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                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                          Length 170245;
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; LOCATION: (1)...(159662)
; COTHER INFORMATION: n = A,'
US-09-947-911-108
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SEQ ID NO 108
LENGTH: 1599662
TYPE: DNA
ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Application US/09947911
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 371; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001300
                                                                                                                                                                                                              1386282 AGGGTGGTCTCAGACTCCTGATGTCAGGTGATCTACCAGCCTCGGCTTCTCAAAGTGCTA 1386223
                                                                  63933 AGAAAATAA 63925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                 184 GAAT-AGTTATAGTGTACCCCATTTACCCATCACTCAGTTTCAACAGCTGGTGACATATT 242
                                                                                                                                                         124 GGATTATAGGCGTGAGCCGCCGCCCAGCCAACATTTTTTAAATACTGAAAAGTAGAGG 183
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                               243 TATTTCTTCTATACCAGTACCGTACTCTCCCCACTGGGATTATTTTAAGGCAAAACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                4 GCCACCATGCCTGGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTGCCATGTTGACC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAAAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATCACTTGAATCCGGGAAGCAGAGATTGCAGTTGAGCTGAGATTGCAGTCGAGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGTTCGAGACCATCCTGGCCAACATGGTGAAAACCCCTGTTTCTACTAAAATACAAAAA 64114
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                                                                                                                                        GGATTACAGGTGTGAGCCACTGCACCCGGCTACAAATTTGTTTTTTTATAATTATAGGTA 1386163
Conservative
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Pred. No. 2.1e-22;
0; Mismatches 210
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1554623)
; OTHER INFORMATION: n = A,T,C or
US-09-947-911-225
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 377; Conservative
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LENGTH: 1554623
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CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 368
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                                                             1429232 GCTTGCACCTGTAATTCCAGCACTTCGAGAAGCTGAGGCAGGTGGATTACCTGAGGTCAG 1429173
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                    241 TTTATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAAACCC 300
                                                                                                                                                                                                                                                                  181 AGGGAATAGTTATAGTGTACCCCATTTACCCCATCACTCAGTTTCAACAGCTGGTGACATA 240
                                                                                                                                                                                                                                                                                                                                                   121 CTGGGATTATAGGCGTGAGCCGCCGCCCCCAGCCAACATTTTTTAAAATACTGAAAAGTAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ATGACATTTTATCCCTAAATACTT-TAGATAAAGGTGTTCTTTGAAAAAAATCATAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCTGCCACCATGCCTGGCTAATTTTCTTÄTTTTTAGTAGAGACGAGGTTTTGCCATGTTG
AGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAA----AAATCAT 356
                                                                                                                                              TTCCCCCATCTCTATAATTTTCTCATTTCAAGAATGCTATATAATGGGCTGGGCATGGTG 1429233
                                                                                                                                                                                                                            GTCACATCTCTTGCCTACTGCCAGTA-TCATCTCTAATCCCTGGAAACAACTGATATA 1429293
                                                                                                                                                                                                                                                                                                          CTTGGATTACAGGCATGAGTCACTGCACCTGGCCTCCCATGTTGGTCTTTTATAGCCACA 1429352
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Pred. No. 3.3e-22;
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US-09-947-911-73

Sequence 73, Application US/09947911

; GENERAL INFORMATION:
; APPLICANT: VERWIER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
; TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001300
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; LOCATION: (1)...(1974088)
; OTHER INFORMATION: n = A,
US-09-947-911-73
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SEQ ID NO 73
LENGTH: 1974088
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                                                                                                                    368563 TCACGCCAGTAATCCCAGCACTTTGGCAGGCCGAAGCTGACAGATCATGAGGTCAGGAGT
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                               121 CTGGGATTATAGGCGTGAGCCGCCGCCACCCAGCCAACATTTTTTAAATACTGAAAAGTAG
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    421
                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCTGCCACCATGCCTGGCTAATTTTCTTATTTTTAGTAGAGACGAGGTTTTTGCCATGTTG
                                    TCAAGACCAACCTGACCAATATGATGAAACCCCATCTCTACCAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                              TCTGGCCCTACACTTTCAGTTCAAAACTCCTGGTAAGTCATCAC - ACTGGGGTAGAAATA
  TTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCA
                                                                                                                                                                                              TTCCTGGAAGCTATTCCTACACCAAGAAGT---CTATGAATAACAGCCCGGCGCTGTGGC
                                                                                                                                                                                                                                     TTTATTTCTTCTATACCAGTACCGTACTCCCCCACTGGGATTATTTTAAGGCAAAACCC
                                                                                                                                                                                                                                                                                                                   AGGGAATAGTTATAGTGTACCCCATTTACCCATCACTCAGTTTCAACAGCTGGTGACATA
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                                                                             TCAGGACCAGCCTGGCCAACATGGTGAAACCCTGTCTGTACTAAAAATACAAAAATTAGC
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Pred. No. 4.3e-22;
0; Mismatches 209;
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PCT-US02-41414-1172/c
Sequence 1172, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEO ID NOS: 1613
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71249/FMS/DCF
CURRENT APPLICATION NUMBER: PCT/US02/41414
CURRENT FILING DATE: 2002-12-26
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LOCATION: (23326)..(24418)
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ORGANISM: Homo sapiens
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                                                                                          GGCAAAACCCCAGATGACATTTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAA
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GGTCAGGAGTTAGAGACCAGCCTGGCCAACATGATGAACCCCCGGTCTCTATTAAAAATAC
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, NAME/KEY: misc_feature
, LOCATION: (1)...(888463)
; OTHER IMPORMATION: n = A,T,C or
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LENGTH: 888463
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
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Best Local Similarity
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CURRENT FILING DATE: 2001-09-07
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                                              594552 CATGGATCACGTGGGGTCAGGAGTTTCAGACCAGCCTGGCCAACATGGTGAAACCCCGTC
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               TGTACTAAAAATAC-AAAAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTAC
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; OTHER INFORMATION: n = A,T,C or
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CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 368
SEQ ID NO 86
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Best Local Similarity
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                                       760540 CTACTAAGAATACAAAAATTAGCTGGGAGTGGTGGCGTGCACCTGTGGTCCCAGCTACTC
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ORGANISM: HUMAN
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  458 AGGAAGCTGAGGCAGGAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGA 517
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58.8%;
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Pred. No. 1.8e-21;
0; Mismatches 252;
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US-10-017-161-2143
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PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED FILE REFERENCE: 084335/0152
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APPLICANT:
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LOCATION:
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LOCATION:
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NAME/KEY: source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
               NAME/KEY:
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LOCATION: (35649)..(35883)
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(6586)..(6893)
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(76611)..(76827)
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(75449)..(75567)
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(62136)..(62275)
                                                                                                                                    (60383)..(60533)
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AKIYAMA, YUTAKA
ABURATANI, HIROYUKI
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APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
ITILE OF INVENTION: METHODS FOR DIAGNOSING RC
FILE REFERENCE: AMIO1055
CURRENT APPLICATION NUMBER: US/60/427,982
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                          RESULT 14
US-60-427-982-322
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                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                            Sequence 322, Application US/60427982
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Best Local Similarity
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                                                                                                                    APPLICANT: Wyeth Research APPLICANT: Burczynski, M
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LOCATION: (99913)..(100084)
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NAME/KEY: CDS
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Pred. No. 4.2e-21;
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; LENGTH: 170245
; TYPE: DNA
; ORGANISM: Homo ;
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                                                                                                                     Sequence 286, Application US/09947911
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version
SEQ ID NO 322
LENGTH: 170245
                                           NUMBER OF SEQ ID NOS: 368
SEQ ID NO 286
LENGTH: 3037227
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                                                                                           CURRENT APPLICATION NUMBER: US/09/947,911 CURRENT FILING DATE: 2001-09-07
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                              TYPE: DNA
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FEATURE:
              ORGANISM:
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Search completed: March 30, 2003, 04:24:50 Job time: 9787.96 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, EMFLGEROFF. THE TEMPLET STATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all the posterior of the correct was finished as follows unless otherwise naturally the content of the correct was finished as follows unless otherwise naturally as the content of the correct was finished as follows unless otherwise naturally as the content of the correct was finished as follows unless otherwise naturally as the correct of the correct was finished as follows unless otherwise naturally as the correct of the correct o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insert of clone RP11-96L14 The true left end of clone RP11-23IP20 is at 72881 in this sequence. The true right end of clone RP11-11ID20 is at 72886 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \ensuremath{\mathtt{RPII}}\xspace^-96\ensuremath{\mathtt{L14}}\xspace is from the library \ensuremath{\mathtt{RPCI}}\xspace^-11.1 constructed by the of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan, cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'-& 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzi
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens cDNA FLJ13429 fis, clone PLACE1002500, weakly similar to Rattus norvegicus zinc transporter (ZnT-2) mRNA. AK023491
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002500.
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Isogai, T. and Otsuki, T.
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663 c 647 g 50
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Quality coverage: 1.63x in Q20 base;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15%, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 22, 2002 this sequence version replaced gi:21068608.
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                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the pieces is not known and their order in this sequence record is
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96 77795: gap of 100 bp
96 80590: contig of 2795 bp in le
91 80690: gap of 100 bp
91 80592: contig of 4362 bp in le
92 85052: contig of 4362 bp in le
153 85152: gap of 100 bp
153 89287: contig of 4135 bp in le
154 89387: gap of 100 bp
155 91754: gap of 100 bp
156 91754: gap of 100 bp
157 91398: contig of 2644 bp in le
158 91564: contig of 2644 bp in le
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96771: contig of 2273 bp
96871: gap of 100 bp
103634: contig of 6763 bp
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11807; cc
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107935: contig of 4201 bp
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25134: contig of 2013 bp
234: gap of 100 bp
28285: contig of 3051 bp
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20654: contig of 2022 bp
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23021: contig of 2267 bp
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18532: contig of 2085 l
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178420: contig of 2310 bp 1
178520: gap of 100 bp
181150: gap of 2640 bp 1
181250: gap of 100 bp
1814022: contig of 2762 bp 1
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248789: contig of 9
248889: gap of 1
250940: contig of 2
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222145: contig of 4
222245: gap of 1
222245: gap of 2
      163242: gap of
265368: contig of
165468: gap of
268121: contig of
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                           Human chromosome 14 DNA sequence BAC R-1017G21 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
AL118558.6
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280983 281082; gap of 100 bp
281083 283442; contig of 2360 bp
283443 283542; gap of 100 bp
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270223: contig of 2002 bp
70323: gap of 100 bp
274441: contig of 4118 bp
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89.8%;
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Pred. No. 4.8e-61;
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AUTHORS
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AUTHORS
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                                                                                                                                     JOURNAL
                                                                                                                                                                                                                   Direct Submission
Submitted (04-SEP-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Sep 6, 2001 this sequence version replaced.gi:14571656.
                                                                                                                                                                                                                                                                                                                                                                                              HTG;
                                                                                                                                                                                                       Unpublished
                                                                                                                                                                       Genoscope.
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                 Center: Genoscope / Centre
Contact: SeqRef@genoscope.cns
                 Web site:
                                    Center code:
                                                                                                                                                                                       (bases 1 to 194871)
                                                                                                                                                                                                                                                                                                                                                                                          8558.6 GI:15485141
HTGS_ACTIVEFIN.
                 http://www.genoscope.cns.fr/
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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Barbe,V., Pelletier,E., Artiguena
ls,T., deBerardinis,V., Cruaud,C.,
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              Identified using the 178326. .178431
                                     dbSTS:STS42866
                                                  /note="matching EMBL:T03672
RHdb:RH53557
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                                                                           Identified using the e-PCR software 178303. .178552
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/db_xref="taxon:9606"
/chromosome="14"
  /note="matching
                                                                                                                                        161688.
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/note="matching EMBL:N46343
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Best Local Similarity
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                                                                                                                                                                                                   SEQUENCE,
AC026091
                                                                                                                                                                                                        Homo sapiens chromosome 17 clone SEQUENCE, 30 unordered minorial process.
Direct Submission
Submitted (19-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 222472)
                                                 Waterston, R.H.
                                                                         Unpublished
                                                                                     The sequence of Homo sapiens
                                                                                                   Waterston, R.H.
                                                                                                                                                  Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT
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178392. .178577
/note="matching EN
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Louis,

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COMMENT
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Insert size: 226258; sum-of-contigs
Quality coverage: 4.24 in Q20 bases; agarose-fp
Quality coverage: 3.81 in Q20 bases; sum-of-contigs
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Chemistry: Dye-terminator Big Dye; 0% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Croke, P., FitzHugh, W., Gage, D., Galagan, J., Bodge, S., Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Tebros, V., Landers, T., Tebros, V., Tebros, V., Landers, T., Tebros, V., Tebros, V., Landers, T., Landers, T., Tebros, V., Landers, T., Landers, T., Tebros, V., Landers, T., Landers
                                                            Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrin,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neil,D., Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 17, clone RP11-661C3 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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56156 c 55982 g 54142 t
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196459. .222472
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177030. .196358
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clone_end:T7
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141115. .158417
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158518. .176929 .
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Pred. No. 3.2
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                                   Norman, C.H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 13, 2002 this sequence version replaced gi:21702875. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roya, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Walson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the finished sequence as soon as it is available the accession number will be preserved.

1 229155: contig of 229155 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project Information Center project name: L12041 Center clone name: 661_C_3
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .229155
                                                                                                                                                     26.0%;
83.8%;
                                                                                                                  0;
                                                                                                                                                     Score 259.8;
Pred. No. 3.2
                                                                                                                      Mismatches
                                                                                                              3.2e-60;
hes 57;
                                                                                                                                                                                       DB 2;
                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185341 GGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCCTGTCTCTACTAAAAAGTACAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662 AATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCA
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AC091504
AC091504.2
  This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                                                                                              Submitted (20-OCT-2001) NIH Intramural Sequencing Grovement Circle, Gaithersburg, MD 20877, USA On Oct 20, 2001 this sequence version replaced gi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (27-APR-2001) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 139130)
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Behjamin, B., Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Behjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Pradad, A., Shevchenko, Y. Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                   Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                     Center project name: aoh
Center clone name: 013M21
                                                                                                                                                                                                                            Contact: nisc_mouse@nhgri.nih.
                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                         Center code: NISC
                                                                                                                                                                                                                                                                                          Center: NIH Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative Sequencing Initiative
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                                                                                                                                                                                                         Project Information
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                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAA 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301;
    1 (bases
Ayele,K.,
                                                       Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                        AC091400.2 GI:14717331
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                   AC091400
                                                                                                                                                                                    Pan troglodytes clone unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE LENGTH: This sequence represents the entire insert of
this clone unless otherwise noted. If there are overlapping
clones, the overlaps are noted in the beginning and end of
                                                                                                                                                                                                                              AC091400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Features section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restriction digest.
                                                                                                       troglodytes.
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139053. .139130
/note="single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="this sequence is not the entire insert of clone RP43-13M21; clone overlaps with GenBank Accession Numbacco91296 (nucleotides 152229-85979) clone RP43-109G19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents overlap with nucleotides 183737-185979 ACC01296"
Eutheria; Primates; Catarrhini; Hominidae;
1 to 173109)
Beckstrom-Sternberg, S.M., Benjamin, B., Blai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:959
/clone="RP43-13M21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RP43"
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Pred. No. 3.6e-60;
0; Mismatches 69;
                                                                                                                                                                                                         173109 bp
RP43-13P21,
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34167 t
                                                                                                                                                                                                         WORKING
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Indels

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linear HTG 1

13-JUL-2001

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65953

Blakesley, R.W.

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JOURNAL
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AUTHORS
TITLE
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be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 150000; agarose-fp
Insert size: 165000; pulse-field-gel
Insert size: 172409; sum-of-contigs
Quality coverage: 12.12x in Q20 bases; agarose-fp
Quality coverage: 11.02x in Q20 bases; pulse-field-gel
Quality coverage: 10.55x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.99031e Consensus quality: 169170 bases at least Q40 Consensus quality: 170155 bases at least Q30 Consensus quality: 170896 bases at least Q20
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Center clone name: 013P21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: NIH Intramural Sequencing Center Center code: NISC
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                     #101. .15655

/note="assembly_fragment"

15756. .27459
                                                                                                                                                                                  /db_xref="taxon:9598"
/clone="RP43-13P21"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
/note="assembly_fragment
                                                                                                  /note="assembly_fragment"
                                                                                                                                                          /clone_lib="RP43"
                                                                                                                                                                                                                                     organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                        15655: contig of 11555 bp in le
15755: gap of unknown length
27459: contig of 11704 bp in le
27459: contig of 11704 bp in le
27559: gap of unknown length
47281: contig of 19722 bp in le
47381: gap of unknown length
70102: contig of 22721 bp in le
70202: gap of unknown length
94878: contig of 24676 bp in le
94978: gap of unknown length
127718: gap of unknown length
127718: gap of unknown length
177109: contig of 45291 bp in le
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Best Local Similarity
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                                                              Muzny, D., Arenson A.D., Brundage, E., Carvelli, K., Chen, E., Chen, J. Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Godman, M., Gorrell, J.H., Haywood, M., Jackson, L., Garcia, C., Godman, M., Gorrell, J.H., Haywood, M., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Timms, K.M., Todd, J., Rowland, K., Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J.
                                                                                                                                                                                                                                                                                               AC003669
                                                                                                                                                                                                                                                                                                                              AC003669 159446 bp DNA linear PRI 24-MAR-19 Homo sapiens \rm Xp22 BAC GS-594A7 (Genome Systems Human BAC library)
 Unpublished 2 (bases 1
                                 Vo,Q., Worley,K.Č., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A. Direct Submission
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                           Homo sapiens
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47382. .70102
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44656 c 43845 g 41916
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27560. .47281
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Pred. No. 3.6
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                                                                   Todd, J.,
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AUTHORS

Worley, K.C

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Submitted (24 MAR-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
On Mar 23, 1998 this sequence version replaced gi:2960508.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exon/Intron boundaries of identified were canonical splice junctions that across the splice junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MAR-1998) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 159446)
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Submitted (09-DEC-1997) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 159446)
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                                                                                                                                                                                                                                      complement(7629. .7716)
/rpt_family="L2"
complement(7876. .8016)
/rpt_family="L2"
                                            complement(10303.
                                                                                                                                                                                            complement(6462. .6488)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                 tyrosine kinase"
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complement(3875. .414
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/rpt_family="MIR"
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1900. .2004
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complement(44. .177)
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                                                           rpt_family="FLAM_C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/rpt_family="LIMC/D"
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/rpt_family=""."
                                                                                                          /rpt_family="LlPA12"
32587. .32619
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29612. .29661
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complement(19857. .20131)

/rpt_family=""""
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25171. .25257
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/rpt_family="MIR"
12793..12912
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complement(32698. .32743)
/rpt_family="AT_rich"
complement(33119. .33163)
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complement(31152. .31
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/rpt_family="MIR"
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N3HPG Homo sapiens cDNA clone 382775 3'"
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complement/nin
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complement(2013)
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complement/oerr
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complement/10275
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/standard_name="HUMSWX1557,
/db_xref="dbSTS:13053"
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)8. .25080
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                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTACTAAAAATACAAAAATTAGCCGGGCTTGGTGGCACATGCCTGTAATCCCAGCTA 113946
                                                                                                                                                                                                                AAAAAAAAGAAAGAAAGAAATCAGAAAT 114094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCTACTAAAAATACAAAAACTAACCAGGCGTGGTGGCTTGTGCCTGTAATCCCAGCTA 640
                                                                                                                                                                                                                                                                                 285;
                                                 HTG;
                                                            Homo sapiens chromosome 17 clone RP11-630D10 map 17, SEQUENCE, 17 unordered pieces.
AC061988
AC061988.2 GI:8084537
                 Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                sapiens.
                                              HTGS_PHASE1; HTGS_DRAFT
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complement(37577. .37620\
/rpt_familv="\"
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43013
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/standard_name="HUMSWX1484, Chr. X, Homo say
/db_xref="dbSTS:13016"
complement(41389._41513)
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37742
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39396. .39468
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/rpt_family="MIR"
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/rpt_family="AT_rich"
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6. .41567
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lement/3657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1 (bases 1 to 165730)
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Consensus quality: 155748 bases at least 040
Consensus quality: 160838 bases at least 030
Consensus quality: 162861 bases at least 020
Insert size: 16200; agarose-fp
Insert size: 164130; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 4.7 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815;
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                                                                         4898 4997; gap of 100 bp 4998 8702; contig of 3705 bp in length 8703 8802; gap of 100 bp 8803 13304; contig of 4502 bp in length 13305 13404; gap of 100 bp 13405 13901; contig of 5887 bp in length 19005 19101 can f
                                                                                                                                                                                                                                                                                           1 1988: contig of 1988 bp in length
1989 2088: gap of 100 bp
2089 4897: contig of 2809 bp in length
4898 4997: gap of 100 bp
4998 8702: contig of 3705 bp in length
     19191: gai
25880:
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                                    gap of
contig of 6689 bp in length
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140744. .165730
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34024 c 33340 g 49137
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120757. .140643
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32809. .39945
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19192. .25880
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8803. .13304
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/clone_lib="RPCI-11 Human Male
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/db_xref="taxon:9606"
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Location/Qualifiers
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AUTHORS
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                                                             Direct Submission
Submitted (05-007-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                             3 (bases 1 to 166424) Waterston, R.H.
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                                                                                                                                                  Waterston, R.
                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                      The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 166424)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                            MO 63108,
                                                                                                                                                                                                                                                                                   Kang, K., Maupin, R.,
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           Center: Washington University Genome (
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Contact: Summary Statistics
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Center project name: H_NH0299I20
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1 to 166424)
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RP11-299120
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BAC clone RP11-299120
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                                                                                                           USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
restriction digest.
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCD. For additional information about the map position of this
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MCD. For additional information about the map position of this

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P., Zhao, B., Frengen, E., Tateno, M., Catanese, J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is ACO24637. Actual start of this clone is at base position 1 of RP11-299120; actual end is at base position 166424 of RP11-299120.

The sequence $H_{\rm N}$ NH0299120 from base position 138712 to 140784 contains a tandem repeat. The tandem size is believed to be agreement with digest information. in

The sequence $H_NH0299120$ from base position 141597 to 143830 contains a tandem repeat. The tandem size is believed to be in agreement with digest information, however, the sequence fidelity cannot be guaranteed.

The sequence H_NH0299120 contains a variable CT run from base position 60019 to 60385. The sequence fidelity cannot be guaranteed

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Homo sapiens BAC clone RP11-353K11
AC092636 AC068117
AC092636.3 GI:19807915
Direct Submission
Submitted (29-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                            Direct Submission
Submitted (10-SEP-2001) Genome
University School of Medicine,
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The sequence of Homo sapiens BAC clone RP11-353K11
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Submitted (16-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                   University, 4444 Forest Park Avenue, St. Louis On Mar 29, 2002 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                    Waterston
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                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                        Drafting Center: WIBR
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This sequence may not represent the entire insert of this
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clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-145M22; the clone sequenced to the right is RP11-219H23. Actual start of this clone is at base position 1 of RP11-353K11; actual end is at base position 199721 of RP11-353K11.

The region from 147655 to 147703; 147819 to 147875 are only covered by pcr products from clone DNA. Single subclone region exist between 147951 and 147966. Polymorphisms exist between AC088539 and AC092636. Data from AC068539 and AC079395 was used to finish AC092636.

The sequence of AC068117 has been incorporated into AC092636 Location/Qualifiers

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            AUTHORS
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                                                                                                                                                                                                                                                                                                                         769
                                                                                                                                                                                                                                                                                                                         AAAAAAAG
                      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadd,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in Database (2000)

2 (bases 1 to 157963)
Hattori,M., Ishii,K.,
Fujiyama,A., Yada,T.,
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                   Homo sapiens
                                                                                                                                              Homo sapiens DNA, clone:RP11-121M22
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Query Match
Best Local Similarity
Matches 277; Conserv
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                                                                                                                                                                                                                                                                                                                               102794 GCTGAGGCACGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 GGCTGGGCACGGTGGCTCATGCCAGCACCTTGGGAGGCTGAGGCAGA 528
                                                                                                                                                                           AAAATAAG 102921
                                                                                                                                                                                                                                                    CCACTGCACTCCAGCCTGGGGGACAGAGCGAGACTCCATCTCAAAAAAATAAAAATAAAAA
                                                                                                                                                                                                                                                                              GCTGAGGCAGGAGATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACA 708
                                                                                                                                                                                                                                                                                                                                                                                                            AAAAATACAAAAATTAGCCAGGCGTGGTGGCATGTGCTTGTAATCCCCCGCTACTCGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACTTGGGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCATCTCTACT 102733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTACT 588
Homo sapiens genomic DNA, chromosome complete sequence. AP002986 AP002986.2 GI:19263031
                                                                              AP002986
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                                                                                                                                                                                                                  776
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/note="similar to Mus musculus EST BI666503

(NID:g15580736)"

14993. .15613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match to EST 14711. .15383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to Mus musculus EST BB653323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14839. .15010
/note="similar to Homo
(NID:g12318197)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Homo sapiens EST AU130216
(NID:g10990570)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(CGCGG)n"
14257. .14300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13845. .14717
/note="CpG_island (%GC=72.2, o/e=0.80, #CpGs=97)"
14085. .14252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14839. .15010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match to EST BE962211 (NID:g11764881)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14307. .14756
/note="match to EST BM147145 (NID:g17166711)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 258.4; DB 9; Pred. No. 7.6e-60;
                                                                            157963 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                          linear PRI 08-MAR-2002 clone:RP11-121M22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 199721;
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Toyoda, A., Taylor, T.D., Hong-Seog, P., Totoki, Y., Watanabe, H. and Sakaki, Y.

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COMMENT
FEATURES
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REFERENCE
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AC023429
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Best Local Similarity
                                                           TITLE
                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81615 AAAAATACAAAAATTAGCCAGGCGTGGTGGCACACGCCTGTAATCCCAGCTACTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81675 TTACCTGAGGTCAAGAGTTCGAGACCAGACCTGGCCAACATGGTGAATCCCCCATCTCTACT 81616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81435 GAAAAGAAAATTGGATCATTTCACTTCTCCATT 81403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 AAAAATACAAAAACTAACCAGGCGTGGTGGCTTGTGCCTGTAATCCCAGCTACTCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 TGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTACT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGAGGCAGGAGAATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACA 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Direct Submission
Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304
                                                                           2 (bases 1 to 170682)
Bruno, D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                  Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hars,N., Herman,Z.S., Hyman,R., Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                          HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC023429 170682 bp DNA linear HTG 10-
Homo sapiens chromosome 11 clone RP11-121M22, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC023429
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                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 170682)
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
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/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-121M22"
36722 c 37247 g 44252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:13569974
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85.9%;
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Pred No. 1.1e-59;
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ORIGIN
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                                                                                                             BASE COUNT
Query Match
Best Local Similarity
Matches 286; Conserv
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                       misc_feature
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Center clone name: RP11-121M22

Center clone name: RP11-121M22

Center clone name: RP11-121M22

Sequencing Vector: M13mp18; X02513

Chemistry: Dye-primer; 12% of reads

Chemistry: Dye-terminator Big Dye; B6% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 165770 bases at least Q40

Consensus quality: 167255 bases at least Q30

Consensus quality: 167255 bases at least Q20

Insert size: 170423; agarose-fp

Quality coverage: 9.0x in Q20 bases; agarose-fp

Quality coverage: 9.1x in Q20 bases; sum-of-contigs.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1857
1957
7066
7166
21090
21190
21146
34146
34246
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109180
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Stanford DNA Sequencing and Technology Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SDSTDC
                                                                                                               clone_end:T7"
39732 c 39
                                                                                                                                                                                                                                       34246. .48562
/note="assembly_name:Contig29
clone_end:SP6"
                                                                                                                                                                                                                                                                                                                                                                               7166.
                                                                                                                                                   109280. .170682
/note="assembly_name:Contig31
                                                                                                                                                                                                                       48663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-121M22"
                                                                                                                                                                                              /note="assembly_name:Contig30
                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI human BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                      25.8%;
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170682: contig of 61403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34245: gap of unknown length 48562: contig of 14317 bp in 48662: gap of unknown length 109179: contig of 60517 bp in 109179:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7165: gap of unknown length
21089: contig of 13924 bp in length
21189: gap of unknown length
34145: contig of 12956 bp in length
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  Score 257.8; DB 2;
Pred. No. 1.1e-59;
0; Mismatches 47;
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Search completed: March 29, 2003, 21:53:09 Job time: 6057.01 secs
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                10045 GAAAAGAAATTGGATCATTTCACTTCTCCATT 10077
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Database
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAK68202	ABA14358	AAL37405	ABK83568	ABA15942	ABK84349	AAK82338	AAK82710	ABA99369	ABA99282	AAK70511	AAS43104	AAD16230	ABL68365	ABL61948	ABL61947	ABA82625	AAK86669	ABK22783	ABL97407	AAL03071	ABA15833	AAC79687	ABK84796	ABK83572	AAK84334	AAH51601	AAS09301	AAS27783	ABL98375	AAK85276	AAL05811	ABA17151	AAS21306	AAK89230	ABA17153
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immune/haema	nervous syst	musculoskele	DNA differen	nervous syst	cDNA differe	immune/haema	immune/haema		ALDH5 DNA.	immune/haema	Oestrogen re	ATP-binding	Kidney cancer rela	adenocarcino	adenocarcino	HBM gene reg	immune/haema	high bone ma	testicular a	reproductive	nervous syst	secreted pro	cDNA differe	cDNA differe	immune/haema	chromosome 1	schizophreni	DNA encoding novel	testicular a	immune/haema	reproductive	nervous syst	cDNA sequenc	ve s	nervous syst

ALIGNMENTS

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RESULT 1
ABN83947
  02-OCT-2002
                         ABN83947;
                                              ABN83947 standard; DNA; 11101
(first entry)
                                                 ВP
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Human transporter protein encoding genomic DNA.

Human; transporter protein; zinc transporter; pharmacogenomic analysis; diagnosis; drug screening; gene therapy; kidney; testis; heart; placenta; small intestine; liver; chromosome 1; single nucleotide polymorphism; gene; ds

Homo sapiens

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exon
              exon
intron
                            intron
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2334..2962
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3184..3735
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2284.2333
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                                                                Location/Qualifiers
                                                            2284..8840
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provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, inappropriate or unwanted expression of the protein. The nucleic acids are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention has been found to be expressed in humans in the kidney, testis, heart, placenta, small intestine and liver. The gene has been localised to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                           The invention relates to an isolated human transporter protein trelated to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease
                                                                                                                                                                                           Novel human transporter proteins, related to zin subfamily, useful as model for developing human serves as target for human therapeutics -
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           TCCTGAAGTCAGACAGCCAGTGCAGGCAGGTCTGGGATTTCTGCCTCATTTCGGTAGACC
                                                              CCATCACTGCTGTCCTGCATTCTTACAGATGAAAAAACAGGCTCAGAGGTTGAATCGTTT
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                                                                                                   GAATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCC
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                                                                                                                                                                                                                    ACTAACCAGGCGTGGTGGCTTGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGA
                                                                                                                                                                                                                                                         AGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTACTAAAAATACAAAA
                                                                                                                                                                                                                                                                   AGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAAACTTCCTACTAAAAATACAAAA
                                                                                                                                                                                                                                                                                                        GCTTTGCCGTATGCCAAGTCCTTACACCCCTCTCAAGAGACAGTCATTGGCTGGGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTACCCAACTACCCCACCCCACCCAAGCCATGGCAGGCCCCAGGAACTTGATCCTGG
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.4e-237;
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RESULT 2

ANHIESON AN
                                                   The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the cc sequence and an oligonucleotide comprising a sequence complementary to a complementary strand of a polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 3'-end sequence, where the cc oligonucleotide comprises a 3'-end sequence, where the cc oligonucleotide comprises a 3'-end sequence, where the cc oligonucleotide comprises a st least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the cd detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13638 and CC AAB95803 represent human amino acid sequences; AAB92446 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001
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, Sugiyama
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; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakama
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Wakamatsu
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A, Nagai I
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(, Otsuki
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                                                      Human;
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                                                                                                                                                                                                GAATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCC
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                                                                        clone (3'-primer)
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                                                     detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                          cDNA;
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                                                                            NO:9257
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07-FEB-2001

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                                                                                                                                                                                                                                                                                                                                                     CC comprises: (a) an oligo-dp primer and an oligonucleotide complementary ctrand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the cC oligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprising a sequence complementary to the cC complementary strand of a polynucleotide which comprises a 5'-end cC sequence and an oligonucleotide comprising a sequence complementary to a C polynucleotide which comprises a '-end sequence, where the cC oligonucleotide comprises a '-end sequence, where the cC oligonucleotide comprises a tleast 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and classification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human amino acid sequences; AAB9246 to CC AAB95893 represent human amino acid sequences; AAB9246 to CC of the present invention.
                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins and full-length cDNAs.
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Ishii
                                                                                                                                                                                                                                                                                                                                 Sequence
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 143
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                                                                                                                                                                                                                    CGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTACTAAAAATACAAAAACTAACC
                                                                                                                        CGTATGCCAAGTCCTTACACCCCTCTCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCA
                           AGGCGTGGTGGCTTGTGTAAT-CCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCG
                                                      CGAGACCAGCCTGGCCAATATGGCGAAACNTCATTTTTACTAAAAATACAAAAACTAGCC
                                                                                                           TGCNTGCAATCCCAGCACCTTGGGAGGCTGAGGCAGGCAGATGACTTGAGGCCAGGAGTT
                                                                                                                                                                NGTATGCCAAGTCNTTACACCCTTNTCAAGAGACAGTCATTGGCTGGGCACGGTGGTTCA
AGGCGTGGTGGCTTGTGCCTGTAATCCCCCAGCTACTCGGGAGGCTGAGGCAGGAGNTTCG
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                                                                                                                                                                                                                                                                                                                                 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                 B₽;
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<sub>1</sub> T, Wakama
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                                                                                                                                                                                                                                                                                       32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   describes primer
                                                                                                                                                                                                                                                                                                                                109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wakamatsu
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                                                                                                                                                                                                                                                                                    Score 326.4;
Pred. No. 5.5
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A, Nagai K,
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                                                                                                                                                                                                                                                                         2;
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84
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                                                      144
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RESULT 4
AAH51627
CC human chromosome 13q31-q33 locus. The nucleotide sequences contain
CC biallelic markers and polymorphisms. Sequences AAH51622 - AAH51626 and
CC AAH62907 - AAH62915 represent cDNA human sbq1 cDNA sequences and protein
CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent q35018
CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used
CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are
CC represented by sequences AH51642 - AAH51699. Nucleotide sequences of
CC amplicons which comprise biallelic markers located on the chromosome
CC are represented in the sequences by degenerate/undefined base codes. PCR
CC primers AAH51818 and AAH51819 are used in the isolation of sequences of
CC the invention. The biallelic marker containing nucleotide sequences of
CC used to determine the identity of the nucleotide at a biallelic marker in
CC a sample DNA sequence. The nucleotide sequences may be labelled and used
CC greated biallelic marker in a biological sample from single or multiple
CC subjects. By determining the frequency of a biallelic marker in a
CC population an association between a genotype and a trait, a haplotype and
CC a trait and a phenotype and a trait can be detected. The sequences can be
          Qy
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27-JUL-1999;
29-JUL-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen D, I
Essioux L;
                                                                                                                                                                                                                                                                                                                                                              Polynucleotides comprising sequences from sbg1 and markers are used for genotyping and detecting schiz disorder and predisposition to these disorders -
                                                                                                                                                                                                                                                                           AAH51601 represents a human genomic nucleotide sequence comprising g34665, sbg2, g35017 and g35018 nucleic acid sequences located on thuman chromosome 13q31-q33 locus. The nucleotide sequences contain
                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                     Page 550-551; 737pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; sbg2; g35017; g35018; chromosome 13q31-q33; haplot marker; polymorphism; schizophrenia; bipolar disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blumenfeld
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990S-0132065.
990S-0143928.
990S-0145915.
990S-0146452.
990S-0146453.
990S-0162288.
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RESULT 5
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Best Local
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27-JUL-1999;
29-JUL-1999;
29-JUL-1999;
                                                                                             Cohen D,
Essioux 1
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                                                                                                                                                                                                                                                                                                                                                         30-MAR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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biallelic marker; po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human g35018 cDNA sequence
  Polynucleotides comprising sequences from
                                                WPI; 2000-619082/59
                                                                                                                                                                 (GEST )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 ACACCCCTCTCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCCAGC 503
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                                                                                                                   Blumenfeld
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99US-0143928.
99US-0145915.
99US-0146452.
99US-0146453.
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olymorphism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%;
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                                                                                                                     Chumakov
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                                                                                                                   Bougueleret
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sbg1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 1301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13q31-q33; haplotype; bipolar disorder; ss.
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g35018 biallelic
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Sequence 1386 BP; 426 A; 319 C; 297 G; 332 T;

12 other;

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amplicons which comprise biallelic markers located on the chromosome 1331-q33 locus are represented in AAH51700 - AAH51817. Biallelic markers are represented in the sequences by degenerate/undefined base codes. PCR primers AAH51818 and AAH51819 are used in the isolation of sequences of the invention. The biallelic marker containing nucleotide sequences are used to determine the identity of the nucleotide at a biallelic marker in a sample DNA sequence. The nucleotide sequences may be labelled and used for genotyping by determining the identity of a nucleotide at a Region D-related biallelic marker in a biological sample from single or multiple subjects. By determining the frequency of a biallelic marker in a population an association between a genotype and a trait, a haplotype and a trait and a phenotype and a trait can be detected. The sequences can be used to determine a predisoposition to or early onset of schizophrenia or bipolar disorder or a beneficial response to or side effects related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018 cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used to isolate sbg1 cDNAs, while sbg1 exons from different primates are represented by sequences AAH51642 - AAH51699. Nucleotide sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the human chromosome 13g31-g33 locus. The nucleotide sequences contain biallelic markers and polymorphisms. Sequences AH51602 - AH51626 and biallelic markers
                                                        treatment against schizophrenia or bipolar disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l represents a human
sbg2, g35017 and g3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 558; 737pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic nucleotide sequence
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Query Match
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CCATCTCAAATTAARAAAAAAAATAAGATACAGAATA
                                                             GAGGTTGCAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGGCCAACAGAGTGAGACT
                                                                                                                            GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTGCTTGAACCTGGGAGGCG
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                             780
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                                                                                                                                                                                                                                                                                                                                                                                      52;
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RESULT 6
AAL07230
Human reproductive system related antigen DNA SEQ ID NO:
                               21-NOV-2001
                                                              AAL07230
                                                                                          AAL07230 standard; DNA; 5881
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                             entry
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Human; reproductive system related cancer; gene therapy; ds.

antigen; reproductive system

disorder;

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17 - JAN - 2000 18 - AUG - 2000 16 - MAR - 2000 24 - FEB - 2000 27 - JUN - 2000 18 - APR - 2000 19 - MAR - 2000 11 - JUL - 2000 10 - JUN - 2000 11 - JUL - 2000 11 - JUL - 2000 11 - JUL - 2000 12 - JUN - 2000 13 - JUN - 2000 14 - AUG - 2000 15 - SEP - 2000 16 - SEP - 2000 17 - SEP - 2000 18 - SEP - 2000 19 - SEP - 2000 11 - SEP - 2000 12 - SEP - 2000 13 - SEP - 2000 14 - SEP - 2000 15 - SEP - 2000 16 - SEP - 2000 17 - SEP - 2000 20 - S	Homo sapiens.
2001WO-US01339. 2000US-01179065. 2000US-0118664. 2000US-01186350. 2000US-01186350. 2000US-01198174. 2000US-01198173. 2000US-01198173. 2000US-0219486. 2000US-0215135. 2000US-0215135. 2000US-021518290. 2000US-0217487. 2000US-0217487. 2000US-0217487. 2000US-0217487. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225275. 2000US-0225266. 2000US-0225759. 2000US	
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29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 02-CCT-2000 02-CCT-2000 02-CCT-2000 02-CCT-2000 03-CCT-2000 03-CCT-2000 04-CCT-2000 05-CCT-2000 06-CCT-2000 06-CCT-2000 06-NOV-2000 06-NOV-2000 06-NOV-2000 06-NOV-2000 06-NOV-2000 06-NOV-2000 07-NOV-2000 08-NOV-2000 09-DEC-2000 09-DEC	26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000;
2000US - 0235367 2000US - 0235367 2000US - 0235369 2000US - 0235369 2000US - 0237039 2000US - 0237039 2000US - 0237040 2000US - 0239935 2000US - 0241785 2000US - 0241787 2000US - 0241809 2000US - 0241809 2000US - 0244617 2000US - 0244617 2000US - 0246476 2000US - 0246476 2000US - 0246476 2000US - 0246611 2000US - 0246526 2000US - 0246526 2000US - 0246527 2000US - 0246521 2000US - 0249211 2000US - 0251186 2000US - 02511869 2000US - 02511989 2000US - 02511989 2000US - 02511989 2000US - 02519199 2000US - 02519199	02335

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RESULT 7
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                                                                                                                                                                                                                                                                                                                          Human; testicular antigen; testes; cancer; metastasis; immune disorde reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
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      31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human testicular antigen encoding DNA fragment SEQ ID NO: 3430
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                                                                                           17-JAN-2001; 2001WO-US01329
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      2000US-0179065
2000US-0180628
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0; Mismatches
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nes 37;
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              Disclosure;
                                         Nucleic acids encoding useful for preventing,
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           3430; 766pp; English
                                         973 human testicular antigen polypeptides, diagnosing and/or treating testicular cancer
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                    Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a prinvolves detecting the level of expression of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; diseas disease progression; drug toxicity; drug efficacy; drug metabol
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298pp; English

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of

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ABK83497/c
ID ABK83497;
XX ABK83497;
AC ABK83497;
XX THUMAN CDNA different
XX Human cDNA different
XX Human; ss; granulocy
XX W viral infection; par
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Best Local
                                    cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel dis Crohn's disease; ulcerative colitis; periodontal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, orgen toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                      viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombos
                                                                                                                                                                                                                                                                                                                                                                               9145
                                                                                                                                                                               Human cDNA differentially expressed in granulocytic cells #68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTAAAAATACAAAAACTAACCAGGCGTGGTGGTGGCTTGTGCCTGTAATCCCAGCTACTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGCTGAGGCAGGAGATCGCTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATCACTTGAGGTCAGGAGTTTGGGACCAGCCTGATCAATATGGTGAAAACCTTGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAAAAAGGAGACCATCACTGCTGCTGCATTCTTACAGATGAAAAAAACAGGCTCA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTAAAAATACAAAAATTAGCCAGGCATGGTGGCGGGCACCTGTGATCCCATCTACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303;
                                                                                                                                            ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                    CDNA; 227968
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77.5%;
                        chronic
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Pred. No. 1.
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                                    inflammatory bowel disease; periodontal disease;
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                                                                                        thrombosis;
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CAAGGCGGGCGGATCACCTGAGGTCAGGÄGTTCGAGACCAGCCTGGCCAACATGGAGAAA TGAGGCAGGCAGATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAA AAAGACAGATATTGGCTGGGTGCAGTGGCTCATGCCTGTAATCCTAGCACTTTGGGAGGC AGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCCAGCACCTTGGGAGGC

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Query Match Best Local Matches

276;

Conservative

0,

Mismatches

44;

Indels Length 0

Gaps

0,

Score 249.6; DB Pred. No. 3e-51;

DB 24; ç;

227968; 0;

Similarity

of the printed specification, but was obtained format directly from WIPO at

in electronic

ftp.wipo.int/pub/published_pct_sequences

227968

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53185 24.98; 86.28;

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(GCA), by detecting the level of expression of gene(s) (Gs) identified by CC DNA chip analysis as given in the specification, and comparing the expression level in an unactivated CC GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent C that alters the expression of at least one gene in Gs; (2) screening (M2) GA by contacting GC with an agent C that alters the expression of at least one gene in Gs; (2) screening (M3) GF an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a C subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially C chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (M3) an inflammation; (M3) an inflammation; (M3) and (M3)
                                                                                                                                   modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 68; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to detecting (M1) granulocyte (GC) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-435328/46
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PR 11-
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31-JAN-2000

04-FEB 2000

24-FEB 2000

16-MAR-2000

17-MAR-2000

19-MAY-2000

07-JUN-2000

28-JUN-2000

07-JUL-2000

07-JUL-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001;
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2000US-0186350
2000US-0189874
2000US-0190076
2000US-0190076
2000US-0209467
2000US-0216486
2000US-0216487
2000US-0216887
2000US-0216887
2000US-0217487
2000US-0217487
2000US-0218290
2000US-0218290
2000US-0224518
2000US-0224518
2000US-0225213
2000US-0225213
2000US-0225213
2000US-0225266
2000US-0225266
2000US-0225267
2000US-02252447
2000US-02252447
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   114-AUG-2000
122-AUG-2000
222-AUG-2000
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239-SEP-2000
249-SEP-2000
259-SEP-2000
269-SEP-2000
270-CCT-2000
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200-CCT-2000
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                                                                                                                                         CC (ABBI-4678-ABBI-8001) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful cc in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly cy
                                              Query Match
Best Local S
Matches 277
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17-NOV
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                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 9484; 1701pp + Sequence Listing; English.
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d metastases
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                                         Score 249.4; DB 2
Pred. No. 1.1e-51;
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04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
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2000US-0179065

2000US-0184664

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2000US-0184664

2000US-0198074

2000US-0198123

2000US-029467

2000US-0214886

2000US-0215135

2000US-02151487

2000US-0215887

2000US-0215887

2000US-0217487

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14-AUG-2000 14-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000

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2000US-0229509 2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231242 2000US-0231243 2000US-0231244 2000US-0231413 2000US-0231414 2000US-0232080 2000US-0232080 2000US-0232080

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17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                       3532
                                                                                                                                                              3592
                                                                                                                                                                                                                                                                                                                                                Sequence 30110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders digestive system, particularly cancer and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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                                                                                                                                                                                      TCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCCAGCACCTTGGGA
AAACCTCATTTCTACTAAAAATACAAAAACTAACCAGGCGTGGTGGTGGCTTGTGCCTGTAAT
                                                                                                                                                              TTAAGATAGTAGCACAGGCTGGACACAGTGGCTCATGCCTGTAATCCCAACATTTTGGGA
                                                                       GGCCGAGGCAGACGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGATG
                                                                                            GGCTGAGGCAGGCAGATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCG
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84.1%;
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2000US-0236367. 2000US-0236368. 2000US-0236369.

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RESULT 12
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                                                               Gerritsen
Smith V,
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   WPI; 2001-408281/43
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                                                               Stewart TA,
                                                                                                    ME,
                                                                                                                           Beresini M,
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2000WO-US00376

2000WO-US03565

2000WO-US03565

2000WO-US04341

2000WO-US04342

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2000WO-US04914

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Tumas D,
                                              Deforge L, Desnoyers L, Flivato
A, Godowski PJ, Gurney AL, Sher
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Matches 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate blological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, preast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, the proliferation of differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511
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                                         GAAAAAACAGGCTCAGAGGTTGAATCGTTTTCCTGAAGTC
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GAAAACAATGTAACTATTTTAAAGTGGTTACATCTATTC
                                                                                     AAAAACTGAAAATAAAAATAAAATATGTATTCTCCTAACTGAAATATTTACTTAATCTG
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76.2%;
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Pred. No. 2.4e-51;
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ABA17151 standard;

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31-JAN-2000
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vulnerary;
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2000US-0249290
2000US-0249216
2000U
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The nucleic acids, proteins, antibodies and (ant)agonists are useful.

In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and orarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

(b) immune disorders e.g. Addison's disease, allergies, autoimmune haproiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 276
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08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                    1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 9482; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers and metastases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  450 CTCTCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCCAGCACCTTG
                                                                                                                                                                                                GCGAAACCTCATTTCTACTAAAAATACAAAAACTAACCAGGCGTGGTGGCTTGTGCCTGT
                                                                                                                                                                                                                                                                                                                                     GGAGGCCGAGGCAGATGACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACGTG
                                                                                                     TAAAAAAAAAAAAAAAAAAAA 772
                                                                                                                                  GCAGTGAGCCAAGATCGCACCACTGCACTCCAGCCTCGGTGACAGAGCAAGACTCCATCT
                                                                                                                                                    GCAGTGAGCTGAGATCACACCACTGCACTCCAGCCTGGGCGACAGAGGCGAGACTCCAGCT
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2000US-0254097.
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85.4%;
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01-SEP-2000

01-SEP-2000
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07-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
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14-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human reproductive system related antigen DNA SEQ ID NO:
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2000US-0190076.
2000US-0190173.
2000US-0205515.
2000US-0219467.
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RESULT 15
AAK85276/c
ID AAK852
XX
AC AAK852
XX
DT 07-NOV
XX
DE Human
XX
KW Human;
KW Cytost
XX
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OS Homo s

AAK85276 standard;

DNA;

3172

ВP

AAK85276;

Human 07-NOV-2001

immune/haematopoietic antigen

(first

entry)

Human; immune; haematopoietic; imm cytostatic; gene therapy; vaccine;

immune/haematopoietic
ine; metastasis; ds.

antigen; cancer; ID NO:40088

genomic sequence

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                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences c number of human reproductive system related antigens. These can k in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoprotein of the invention.
                                         2459
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                                                                                                                                                                                                                                                                                         Sequence 3172 BP; 1024 A; 529 C;
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05-JAN-2001;
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CAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGGAGGCAGAGGTTGCAGT
                                                                                                                        CTGAGGCAGGCAGATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAA
                                                                                                                                                                                                                    AAGAGACAGTCATTGGCTGGGCACGGTGGCCTCATGCCTGCAATCCCAGCACCTTGGGAGG
                                                             GAGCTGAGATCACCACCACCTCCAGCCTGGGCGACAGAGCGAGACTCCAGCTTAAAA
                                                                                CAGCTCCTTGGGAGGCTGAGGCAGGAGAATCTCTTGAACCTGGGAGGAAGAGATTGCAGT
                                                                                                                                                                  CAGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAA
                                                                                                                                                                                                          AAAAAAAAAAGAGGCTGGGTGCGGTGCCTCACGCCTATAATCCCAGCACTTTGGGAGG
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2000US-0251479.
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2000US-0251869.
2000US-0251990.
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                                                                                                                                                                                                                                                0;
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Pred. No. 2.4e
0; Mismatches
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2.4e-51;
3 47; Indels
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Search completed: March 29, 2003, 17:41:04 Job time: 780.075 secs

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ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AU156173/c LOCUS DEFINITION
Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of	. Y., Nagal,T., Sugano,S., Isogal,T.) Unpublished (2000) Contact: Takao Isogai	rumamo Co, o., Wakamacsu, A., Ozawa, M., Nakamura, I., Nagari, I., Sugaro, S. and Isogari, T.). HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura	Mammalia: Butheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 401) 1 (bases 1 to 401) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Venemoro, T. Pakemater, A. Ozawa M. Nakemura Y. Nagai T. Groano	sequence. AU156173 AU156173.1 GI:11017694 EST. human. Homo Sapiens	AU156173 AU156173 PLACE1 Homo sapiens cDNA clone PLACE1002500 3', mRNA

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                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer R
                                                                                                                           l (bases 1 to 624)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                EST.
                                                                                         sequence tags
                                                                                                     Shotgun sequencing of the human transcriptome with ORF
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/clone="pLACE1002500"
/clone_lib="pLACE1"
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/note="Vector: pME18SFL3"
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Query Match
Best Local Similarity
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Fujiyama,A., Hattori,M., Toyo
Totoki,Y., Watanabe,H. and Sa
BAC end sequences of Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 8
High quality sequence stop: 623
Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer
Project. This entry can be seen in the following URL
                                                                                                                                                             Pan troglodytes male lymphocytes DNA, Male BAC Library clone:RP43-014K03.TJ
                                                                                                                                                                                                                                    AG151502
AG151502.1
                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                    sequence.
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261200-003-f06&t3=2000-12-26&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="EN0092"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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84.5%;
                                                                                            Chordata;
Primates;
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Pred. No. 1.4e-26;
0; Mismatches 52
                       Toyoda, A.,
nd Sakaki, Y.
                                                                                                                                                                                                                                                                                                         RP43-014K03.TJ,
                                                                                            Craniata; Vo
Catarrhini;
                                             Taylor, T.D.,
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                                                                                                                                                                                       clone_lib:RPCI-43 Chimpanzee
                                                                                                                  Vertebrata;
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Matches 280; Conserv
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                                                                                                                                                                                                                                                                                                                                     AAAAAATAAACTGAATATTCCAGTGGT 101
                                                                                                               B59854.1
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes9cs.riken.go.jp, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 642)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linl, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya
                                                                                                                                                                            B59854 642
CIT-HSP-345H13.TVB CIT-HSP HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end was generated during the R&D process and may have higher chance of clone tracking errors. 
 \ensuremath{\mathsf{PRIMERS}}
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Totoki,Y., Watanabe,H.
                                                                                human
Homo sapiens
                                                                                                                                              sequence.
B59854
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LIBRARY
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R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
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/celne_lib="RPCI-43 Chimpanzee Male
/state="language: 137 c 147 g 190 t
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/db_xref="taxon:9598"
/clone="RP43-014K03.TJ"
/sex="male"
                                                                                                                                 GI:2614572
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Shizuya, H., Simon,
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                                                                Euteleostomi;
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                                                                                                                                                                                                                                                                                                                        CCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGGAGGCAGAGGTTGCAG
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                                                                                                                                                                                                                            AAAAAAAAAAAAAAAAAAAAGGAGA
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                                                                                        AGENCOURT_6459887 NIH_MGC_92
5', mRNA sequence.
BM802793
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are available from
end search page:
http://www.tigr.org/tdb/hu
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                        Homo sapiens
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Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
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                                                      human
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/clone="345H13"
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/db_xref="GDB:5363319"
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/note="Vector: pBeloBAC11; Site_1:
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85.3%;
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DNA sequence.
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                             AQ415030
RPCI-11-203E3.TV RPCI-11
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plate: LLAM12324 row: n column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."

a 372 c 303 g 188 t 1 others
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/clone="IMAGE:5575110"
/clone_lib="NIH_MGC_92"
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                                  AAAAAAAAAAAAAAAAAAAAGGAGA 780
                                                                                                                        GAGCCGAGATCATGCCACTGCACCCTGGGCGACAGAGCCAAGACTCCATCTCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu/ordering) or from
(pacpac.med.buffalo.edu/ordering) or from
(pacpac.med.buffalo.edu/ordering)
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Other_GSSs: RPCI-11-203E3.TJ
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1 (bases 1 to 711)
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/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: Ec
/note="Vector: BAC Library"
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/db_xref="taxon:9606"
/clone="RPCI-11-203E3"
/clone_lib="RPCI-11"
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               755 AAAAAAAAAAAAAAAAAAAA 775
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                                                                                                                                                                                                                     255 ACCCCGGCTCTACTAAAAATACAAAAATTAGCCAGGCCTGGTGGTGTGCAGCTGTAATCC
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75
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 634 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 358.
                                                                                         GAGCTGAGATCACACCACTGCACTCCAGCCTGGGCGAGACAGAGCGAGACTCCAGCTTAAAA
                                                                     GAGCTGAGATCGTGCCACTGCATTCCAGCCTGGGTGACAGAGTGAGACTCCATTTCAAAA
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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439 bp mRNA linear EST 19-P mg70f04.51 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:94015 similar to contains Alu repetitive element; contains element repetitive element; mRNA sequence.

AA515728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:940159"
/clone_11b="NCI_CGAP_L1p2"
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/lab_host="DH10B"
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                                                                                                                        GGCTGAGGCAGGAGATAGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCAAGATCAC
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                                                           ACCACTGCACTCCAGCCTGGGCAACAGAGCAAGATTCCGTCTCAAAAAATAAAATAAAAT
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B15692
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Class: BAC ends.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C. Use of a BAC End Sequence Database for Sequence-Ready Unpublished (1997) Other_GSSs: 345N08.TV 345N08.TVB
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301 838 0208
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CalTech Human BAC Library A1"
96 c 114 g 104 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="A-345N08"
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Insert Length: 554 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 430)
NCI-CGAP http://www
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="infiltrating ductal carcinoma"
/lab_host="DH10B"
/note="Organ: breast; Vector: pAMP10; mRNA made from
infiltrating ductal carcinoma, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. "
a 103 c 125 g 89 t
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Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:1386688"
/clone_lib="NCI_CGAP_Br5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Arcaro MA, Morley M, Burdick J, Department of Pediatrics University of Pennsylvania 3516 Civic Center Blvd, ARC 516, Philadel Tel: 215 590 2664
Fax: 215 590 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 bp UP_503-13K_T7 RPCI11 Human Male clone 503-13K, DNA sequence BH367159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mlennox@mail.med.upenn.edu
plate: 503 row: K column: 13
Seg primer: T7
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Raap, A.K., Morley, M.
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/note="Vector: pBACe3.6; RPCI11 Human Male
109 c 83 g 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="503-13K"
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AL704074 530 bp
DKFZp68601228_rl 686 (synonym: h
DKFZp68601228 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 782)
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Plate: LLAM10636 row: h column: 15
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/clone_lib="NCI_CGAP_Skn3"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH1OB (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/db_xref="taxon:9606"
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AL704074.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Ottenwaelder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ottenwaelder, B., Obermaler, B.,
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Mammalia;
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 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available.
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cDNA-collection"
130 c 101 g 183 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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 657 L
B CIT-HSP Hom
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Primates;
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Pred. No. 1.2e-25;
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                57 bp
Homo
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                sapiens
                                 DNA
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genomic cl
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                  clone
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                GSS 21-JUN-1998
ne 2017C7, DNA
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                                                                        AAAAAAAAAAAAAGGAGACCATCACTGCTGCTGCATTCTTACAGATGAAAAAACAGG
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                           CTCAGAGGTTGAATCGTTTTCCTGAAGTCA 851
                                                       CTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGTGTGTGCCTGTAATCCCAGCTAC
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CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                              AGGCGGATCACCTGAAGTCAGGAGTTGGAGACCAGCCTGGCCAACATGGTGAAACCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                  300;
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B65134.1
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linh, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are available from Research
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/db_xref="GDB:7043769"
/db_xref="taxon:9606"
/clone="2017C7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Sperm"
/note="Vector: pBeloBAC11;
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76.9%;
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Pred. No. 1.2e-25;
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Suh,E., Wible,C., Shizuya,H., Simon,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (info@resgen.com).
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RESULT 15
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Matches 280
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UI-H-DTO-avi-b-08-0-UI.s1 NCI_CGAP_DTO i
IMAGE:5879719 3', mRNA sequence.
BM99332
BM993321 GI:19712767
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.
Quackenbush, J.
Quackenbush, J.
Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: John Quackenbush
Contact: John Quackenbush
The Institute for Genomic Research
0712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr.,
Tel: 301 838 3528
Fax: 301 838 0208
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: johng@tigr.org
Plate: 279
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AW970571.1
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
128 c 141 g 89 t
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Yeatman,T.J.
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KEYWORDS VERSION

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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ALIGNMENTS

GENERAL INFORMATION: APPLICANT: BOUGUELETET, LYGIE APPLICANT: BOUGUELETET, LYGIE TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH FILE REFERENCE: GENSET.031A CURRENT APPLICATION NUMBER: US/09/345,882 CURRENT FILING DATE: 1999-06-30 PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30 PRIOR FILING DATE: 1998-06-30 ORGANISM: Homo sapiens FEATURE: NAME/KEY: allele LOCATION: 72794 OTHER INFORMATION: 5-12/FEATURE: FEATURE: NAME/KEY: allele LOCATION: 93714 OTHER INFORMATION: (FEATURE: NAME/KEY: allele LOCATION: 90842 OTHER INFORMATION: 9 PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 140 SOFTWARE: Patent.pm NAME/KEY: allele LOCATION: 97122 OTHER INFORMATION: OTHER INFORMATION: 5-130-257 NAME/KEY: allele LOCATION: 99098 OTHER INFORMATION: NAME/KEY: allele LOCATION: 97152 OTHER INFORMATION: NAME/KEY: allele LOCATION: 88073 5-124-273 : 5-129-144 99-1442-224 5-128-60 99-1437-325 5-127-261 •• .. •• polymorphic polymorphic polymorphic polymorphic polymorphic polymorphic polymorphic base base base base base base base deletion × Þ Þ deletion G Þ or or S or or Or. റ C G BINDING PROTEIN (RBP-SAID NUCLEIC ACID. н of G of. G н

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LOCATION:
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LOCATION: 99094..99140
OTHER INFORMATION: pol:
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LOCATION: 106918..106966
OTHER INFORMATION: polym
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic
           NAME/KEY:
                        FEATURE:
                               LOCATION: 108084...
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 106918
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LOCATION: 99075..99
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LOCATION: 99075..99121
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NAME/KEY: allele
LOCATION: 97130..97177
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NAME/KEY: allele
LOCATION: 97130..97177
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OTHER INFORMATION:
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LOCATION: 93690..93736
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LOCATION: 93690..9
OTHER INFORMATION:
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Best Local Similarity
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                                                                                     CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
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TELEPHONE: 610-27
TELEFAX: 610-27
INFORMATION FOR SEQ
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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                                                    REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STATE: Pennsylvania
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FILING DATE: 26-MAY-1995
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Pred. No. 4e-57;
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Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08451778A Patent No. 5830649
PILING DATE: 26-WAY-1955
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P502
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5364
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LENGTH: 7676 base pairs
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5765 AGAAAGAAAGAAAGA 5747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Galactokinase NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 AGTCATTGGCTGGGCACGGTGGCTGATGCCTGCAATCCCAGCACCTTGGGAAGGCTGAGGC
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                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
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                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                             Version #1.30
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RESULT 4
US-08-998-208-7/c
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                                        APPLICATION NUMBER: 08/451,777
FILING DATE: 26-WAY-1995
APPLICATION NUMBER: PTC/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Galactokinase NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bergsma, Derk J. APPLICANT: Stambolian, Dwight
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                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           NAME: Eagle, Alissa M. REGISTRATION NUMBER: 3
                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                FILING DATE:
                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
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270; Conserv
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NUMBER:
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P50268-1B
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Pred. No. 4.6e-57;
0; Mismatches 49
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CLASSIFICATION: PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

PCT/US95/06743

Version

FILING DATE: 23-SEP-1994 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: REFERENCE/DOCKET NUM

NUMBER:

P50268-1

NAME:

Sutton, Jeffrey A.

APPLICATION NUMBER: PCT, FILING DATE: 23-SEP-199

PCT/US94/10825

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PCT-US95-06743-7/c
Sequence 7, Application PC/TUS9506743
GENERAL INFORMATION:
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Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELEFAX: 610-270-5090
                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                         TITLE OF INVENTION: Human Galactokinase NUMBER OF SEQUENCES: 32
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MOLECULE TYPE:
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                                                                                                                     STATE:
                                                                                                       COUNTRY:
                                                                                                                                 CITY: King of Prussia
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                                                                                                                                                                 Intellectual Property
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity 84.0
Matches 270; Conservative
                                                                                                                                                                                                     SEQ ID NO
                                                                                                                                                                                                                                                                                    APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A
TITLE OF INVENTION: AND POLYMORPHIC MARKERS
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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               FEATURE: NAME/KEY:
                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                              NAME/KEY: allele LOCATION: 72794
                                          OTHER INFORMATION:
                                                     NAME/KEY: allele
LOCATION: 88073
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                                                                                                 OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION:
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NAME/KEY: allele
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OTHER INFORMATION: !
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 108149
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NAME/KEY: 99094 . 99140
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NAME/KEY: allele
LOCATION: 103783...
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OTHER INFORMATION:
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LOCATION: 93690..93736
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LOCATION: 90819..90865
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OTHER INFORMATION:
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LOCATION: 93690..93736
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LOCATION: 90819..90865
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97130..97177
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RESULT 7
US-08-969-125-8
; Sequence 8, Application US/08969125B
; Patent No. 6143871
; Patent NO. 61438710N:
; GENERAL INFORMATION:
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Best Local Similarity
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LOCATION: 108084...
OTHER INFORMATION:
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LOCATION: 108084..108130
OTHER INFORMATION: polymorphic
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LOCATION: 108127
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LOCATION: 106918..106966
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LOCATION: 106918..106966
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ZIP: 222U1-4...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                          TITLE OF INVENTION: SUBST
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
STREET: 1100 NORTH G
                                                                                                                                                                   APPLICANT: BONNEFOY,
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                                           COUNTRY: U.S.A. ZIP: 22201-4714
                                                                   CITY: ARLINGTON
STATE: VIRGINIA
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Pred. No. 5.8
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OPERATING SYSTEM: PC-DOS/MS-DOS

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US-09-800-960-3/c
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                                                                             GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLAT
TITLE OF INVENTION: ACID M
TITLE OF INVENTION: THEREO
                                                                                                                                                                   Sequence 3, Application US/09800960 Patent No. 6387677
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CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            2014
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les 269; Conserv
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APPLICATION NUMBER: US/08/969,125B
FILING DATE: 12-No. 6143871-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 43..1323
SEQUENCE DESCRIPTION: SEQ ID NO:
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LENGTH: 4038 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              AAAAAAAAGGAGACCATCACT 788
                                                                                                                                                                                                                                                                                                                                                                                                          AAGCTGAGGCAGGTGAATTGTTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCAGAGATCA
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STRANDEDNESS: single
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
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TELEFAX: (703) 816-4100
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                                                                                    ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3
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; LOCATION: (1)...(62804
; OTHER INFORMATION: n =
US-09-800-960-3
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US-09-729-995-3
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APPLICANT: WEI, Ming-Hui et al
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Patent No. 6426206
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Best Local
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Best Local Similarity
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TITLE OF INVENTION: ACID MOLECULES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000904
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT FILING DATE: 2000-12-06
                                                                                                           48901 AGGCGGGTGGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48961 ACATGGTGGGTGGGCACGGTGGCTCACACCTGTAATCTCAGCACTTTGGGAGGCCA 48902
                                               11691 CACCTGAGGTCAGGAGTTCAAGACCAGCCTGACCAACATGGCGAAACCCTGTCTCTACTA 11750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                530 GACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTACTA 589
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                                                                                                                                                                          Local Similarity
nes 267; Conserv
AAAATACAAAAACTAACCAGGCGTGGGTGGCTTGTGCCTGTAATCCCAGCTACTCGGGAGG
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                                                                                                                                                                        Score 237; DB 4; I
Pred. No. 8.5e-56;
0; Mismatches 50;
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Pred. No. 1.1e-55;
0; Mismatches 58;
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RESULT 11
US-09-078-294-9/c
Sequence 9, Application US/09078294
Patent No. 6265211
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US-09-851-896-3/c
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Best Local S
Matches 277
 GENERAL INFORMATION:
APPLICANT: Choo, KOO
APPLICANT: Du Sart,
APPLICANT: Cancilla
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CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 70000
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
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                                                                                                                                            TCTCAAAAAACAAAACCAAAACCAAAAATAAAGAGCCAGGGCT 11833
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Choo, Kong-Hong Andy
Du Sart, Desiree
Cancilla, Michael R.
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Pred. No. 1.4e
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                             CACCTTGGGAGGCTGAGGCAGGCAGAGTGACTTGAGGCCAGGAGTTCGAGACCAGGCCTGGC
                CACTTTGGGAGGCTGAGGCAGGAGGAACACCTGAGGTCAGGAGTTTGGGACCAGCCTGGC
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RESULT 12
US-09-735-934A-3
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; ORGANISM: BAC-F2
US-09-078-294-9
                                                                                                                                           US-09-735-934A-3
                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09735934A Patent No. 6372468 GENERAL INFORMATION:
APPLICANT: LI, Jiayin et al
                                                                                                                                                                                                              SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 9
                                                                                                     Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                             FILE REFERENCE: CL000851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEILE OF INVENTION: THEREOF
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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441 CTTACACCCCTCTCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCC
                                                                    Local Similarity 80.7 ses 276; Conservative
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                                                                   Score 236.4; DB 4;
Pred. No. 1.5e-55;
0; Mismatches 66;
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Pred. No. 3.4e-56;
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US-08-480-784-20/c
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                                                                                                                                                                                                                                                                                       PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/300,266
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 08/308,104
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 202-962-4810
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                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 29-NOV-1994
                                               NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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Goldgar, David I
Miki, Yoshio
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Shattuck-Eidens, Donna
Tavtigian, Sean V.
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US-08-483-553-20/c
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APPLICANT: Skolnic
APPLICANT: Goldgar
APPLICANT: Miki, Y
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                            TITLE OF INVENTION:
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APPLICATION DATA:
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Shattuck-Eidens, D
Tavtigian, Sean V.
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Miki, Yoshio
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              PatentIn Release #1.0,
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Susceptibility Gene
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Suite 1000
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           Sequence 20, Application US/08487002 Patent No. 5710001 GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
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ORGANISM: Hom
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 APPLICANT:
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APPLICATION NUMBER:
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Shattuck-Eidens, Donna M.
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Pred. No. 7.2e-56;
0; Mismatches 48
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                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                               5685
                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOR
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0: FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                               5745
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APPLICATION NUMBER:
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             588 TAAAAATACAAAAACTAACCAGGCGTGGTGGCTTGTGCCTGTAATCCCAGCTACTCGGGA 647
                                                                                               528
                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/348,824 FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1201 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/487,002
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STREET: 1201 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
TAAAAATACAAAAATTAGCCGGGTGTGGTGGCGCGCGCCTGTAGTCCCAGCTACTAGAGA
                                                               ACCACTTGAGGTCATGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTAC
                                                                              ATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCTAC 587
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Durocher, Francine
IVENTION: 17q-Linked Breast and Ovarian Cancer
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SYSTEM: PC-DOS/MS-DOS
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ER: 24884-109347
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Pred. No. 7.2e-56;
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Suite 1000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                          Score
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       Published_Applications_NA:*
|: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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           0 US-09-880-107-3327
US-10-128-072-125
US-10-121-049-125
US-10-123-904-125
US-10-123-904-125
US-10-176-918-125
US-10-176-918-125
US-10-176-921-125
US-10-176-921-125
US-10-176-921-125
US-10-140-474-125
US-10-142-431-125
US-10-142-419-125
US-10-142-42-125
US-10-142-43-125
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Sequence 3327, Ap
Sequence 125, App
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240. 240. 240.	240.8 240.6 240.6	241.2 241 241 241 240.8	241.6 241.4 241.2	242.2 242 242 241.6	244 244 243.2 243.2 243.2 243.4	247.8 245.2 244.2
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US-09-962-436-306 US-09-880-107-2225 US-09-880-107-1542	US-09-764-847-1141 US-09-880-107-2378 US-09-880-107-2228	US-09-764-847-1132 US-09-764-877-2680 US-09-967-768A-314 US-10-092-154-1141	US-09-764-877-2419 US-09-764-860-797 US-10-092-154-1132	US-09-967-768A-116 US-09-854-883-243 US-09-820-002-3	US-10-080-644 1 US-09-819-994-3 US-09-835-232-7 US-09-967-768A-314 US-09-982-091A-5 US-09-982-091A-5 US-09-982-246-3 US-09-764-877-3220	US-09-859-888-3 US-09-764-877-3770 US-09-800-729-32
306, 2225, 1542,	Sequence 1141, Ap Sequence 2378, Ap Sequence 2228, Ap	Sequence 1132, Ap Sequence 2680, Ap Sequence 314, App Sequence 1141, Ap	Sequence 2419, Ap Sequence 797, App Sequence 1132, Ap		Sequence 1, Appli Sequence 3, Appli Sequence 7, Appli Sequence 314, App Sequence 5, Appli Sequence 3, Appli Sequence 320, An	Sequence 3, Appli Sequence 3770, Ap Sequence 32, Appl

ALIGNMENTS

RESULT 1 US-09-880-107-3327/c

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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Horne, I
APPLICANT: Vockley
APPLICANT: Scherf,
APPLICANT: Gene Lo
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Best Local Similarity
Matches 303; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 40433
TYPE: DNA
                                                                       9445
                                                                                                                                                9505 ACTGGCTGGGCACGGTGGCTCATGCCTGCAATCCTAGCACTTCGGGAGGCTGAGGTGGGC
                                                                                                                                                                   ACTAAAAATACAAAAACTAACCAGGCGTGGTGGTGTTGTGCCTGTAATCCCAGCTACTCGG
                                                                                          AGATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGGCGAAACCTCATTTCT 585
ACTAAAAATACAAAAATTAGCCAGGCATGGTGGCGGGCACCTGTGATCCCATCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                       AGATCACTTGAGGTCAGGAGTTTGGGACCAGCCTGATCAATATGGTGAAACCTTGTCTCT
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                                                                                                                                                                                                                       Conservative
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77.5%;
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Pred. No. 3.7e-64;
0; Mismatches 88;
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US-10-028-072-125
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TITLE OF INVENTION:
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             OR APPLICATION NUMBER: 60/059836
OR FILING DATE: 1997-09-24
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR APPLICATION NUMBER: 60/062287
OR APPLICATION NUMBER: 60/062287
OR FILING DATE: 1997-10-17
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OR APPLICATION NUMBER: 60/049911
OR FILING DATE: 1997-06-18
OR APPLICATION NUMBER: 60/056974
OR FILING DATE: 1997-08-26
OR APPLICATION NUMBER: 60/059113
OR FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                APPLICATION NUMBER: 60/059184
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
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FILING DATE:
APPLICATION N
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Filvaroff, Ellen
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Watanabe,Colin K
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-02-27
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APPLICATION NUMBER: 60/069212
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RESULT 3
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; Publication No. US200:
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    The Result INFORMATION:
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                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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Gurney, Austin L.
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Filvaroff, Ellen
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Godowski, Paul
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76.2%;
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 Score 248; DB 9; 1
Pred. No. 6.2e-64;
0; Mismatches 95;
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TTTTAAAATATGTACTCTGGCCGGTTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGG

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                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo
US-10-123-904-125
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; Sequence 125, Application US/10123904

; Publication No. US20030022328A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
                                                                                                                                                                                               Prior Application removed
NUMBER OF SEQ ID NOS: 550
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                                                                         Similarity
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Godowski, Paul J.
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                                                           Conservative
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76.2%;
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                                                         Score 248; DB 9;
Pred. No. 6.2e-64;
0; Mismatches 95
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; ORGANISM: Homo
US-10-140-470-125
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LENGTH: 4374
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                                                                                                                                                                                                         Query Match
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CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                        Local Similarity
                                                                                                                       TCTCAAGAGACAGTCATTGGCTGGGCACGGTGGCTCATGCCTGCAATCCCAGCACCTTGG
 CGAAACCTCATTTCTACTAAAAATACAAAAACTAACCAGGCGTGGTGGCTTGTGCCTGTA 630
                                   CAGGCCGAGATGGGCGGATCTTTTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGG
                                                     GAGGCTGAGGCAGATGACTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAATATGG
                                                                                                     TTTTAAAATATGTACTCTGGCCGGTTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGG 3171
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Zhang, Zemin
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Watanabe, Colin K
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Pred. No. 6.2e-64;
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Sequence 125, Application US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
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; ORGANISM: Homo Sapien
US-10-175-746-125
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LENGTH: 4374
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Gerritsen, Mary E.
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US-10-176-918-125
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SEQ ID NO 125
LENGTH: 4374
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CURRENT FILING DATE: 2002-06-20
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; ORGANISM: Homo Sapien
US-10-176-921-125
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 125
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CURRENT FILING DATE: 2002-06-20
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Gurney, Austin L.
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DeForge, Laura
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NUMBER OF SEQ ID NOS: 550
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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Sherwood, Steven
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NUMBER OF SEQ ID NOS: 550
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Sequence 125, Application US/10142431 Publication No. US20030036179A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
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Sherwood, Steven
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RESULT 12 US-10-143-114-125

Sequence 125, Applic Publication No. US20 GENERAL INFORMATION:

Application US/10143114 o. US20030036180A1

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APPLICANT: Baker, Kevin P APPLICANT: Beresini, Mau APPLICANT: DeForge, Laur APPLICANT: Desnoyers, Lu APPLICANT: Filvaroff, El

Desnoyers,Luc DeForge, Laura Beresini, Maureen

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Best Local Sin
Matches 305;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 125
LENGTH: 4374
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CURRENT FILING DATE: 2002-05-10
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ORGANISM: Homo
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GAAAACAATGTAACTATTTTAAAGTGGTTACATCTATTC
                        GAAAAAACAGGCTCAGAGGTTGAATCGTTTTCCTGAAGTC
                                                         AAAAACTGAAAATAAAAATAAAATATGTATTCTCCTAACTGAAATATTTACTTAATCTG 3471
                                                                                                                                                CAGTGAGCTGAGATCACCACCTGCACTCCAGCCTGGGCGACAGAGCGAGACTCCAGCTT
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                                                                                     Similarity
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Gerritsen, Mary E.
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76.2%;
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Pred. No. 6.2e-64;
0; Mismatches 95
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RESULT 13
US-10-140-002-125
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-143-114-125
                                                                                                                            GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 125
                                                APPLICANT:
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Desnoyers, Luc
Filvaroff, Ellen
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Gurney, Austin L.
Sherwood, Steven
Godowski, Paul
Gurney, Austin
                                    Gerritsen, Mary E
                                                Gao, Wei-Qiang
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Wood,William
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Goddard, Audrey
                       Goddard, Audrey
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                                                                                                                                        Application US/10140002 o. US20030037623A1
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Pred. No. 6.2e-64;
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RESULT 14
US-10-142-419-125
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LENGTH: 4374
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood,William
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Smith, Victoria
Stewart, Timothy
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Filvaroff, Ellen
Watanabe, Colin
                                           Stewart, Timothy A.
                                                                      Smith, Victoria
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                        Tumas,Daniel
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APPLICANT:

Wood, William

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: Sequence 125, Application US/10123262

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R10244

CURRENT PILING DATE: 2002-05-10

Prior Apploication number: US/10/142,419

CURRENT FILING DATE: 2002-05-10

Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550

SEQ ID NO 125

LENGTH: 4374

TYPE: DNA

ORGANISM: Homo Sapien
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        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                           Tumas, Daniel
Watanabe, Colin K
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Godowski, Paul J.
Gurney, Austin L.
                                             Zhang, Zemin
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Filvaroff, Ellen
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SUMMARIES

Result No. 38 444 443 443 443 363.6 363.6 350.6 346 251.8 1197.4 1184.2 1177.2 1176.2 1175.6 1152.6 1152.6 1152.6 100 79 78 50 46 45 37 Query Match 111. (110. 9 10. 9 10. 3 10. 3 9 . 4 9 . 4 9 . 4 9 . 4 9 . 3 .7 26209 1 81100 1 171134 1 174314 1 307911 1 1083 3 110000 1 72421 2 138537 2 138537 1179 160040 174303 240125 5422 5422 153241 198220 11101 176006 1952 2000 2101 2823 2852 DВ 96990 10 10 AX086187 HSM803077 AC109690 AC102314 HSA337344 HSA337349 HSA337305 D AF003747 BC026089 RNY16774 AK023491 AK023504 AX411375 AL391650 MMU76007 HSU76010 AX411373 BC006251 AX405563 AY044454 CEY111B2__ AC101509 AC130608 AC130598 AC130598 HSA331528 AY044452 AC105674 CEY39E4A AC019838 AC009198 AC011066 AE003635 AF025409 AY071460 HSU76010 BC028358 AX061210 AX351593 AK094027 U76007 Mus musculu U76010 Human putat BC028558 Homo sapi AX061210 Sequence AX351593 Sequence AX351593 Sequence AX351593 Sequence AX1713790 Homo sapi AC109590 Rattus no AC102314 Mus muscu AJ337087 Homo sapi AJ337944 Homo sapi AJ337944 Homo sapi AJ337957 Homo sapi AJ337974 Rattus nozv BC026089 Homo sapi AF025409 Homo sapi AF044454 Thlaspi AF044452 Thlaspi AX411373 Sequence BC006251 Homo sapi AX405563 Sequence AK094027 Homo sapi BC013478 Mus muscu U50927 Rattus norv AK023491 Homo sapi AX411375 Sequence AL391650 Human DNA AY044453 Thlaspi g AL138642 Arabidops Description

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AUTHORS Wei, M.H., Ketchum, K.A., di Francesco, V. and Beasley, E.M.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1	ORGANISM Homo sapiens	SOURCE human.	KEYWORDS .	VERSION AX411373.1 GI:21444024	ACCESSION AX411373	DEFINITION Sequence 1 from Patent W00224910	LOCUS AX411373	AX411373	RESULT 1
Wei,M.H., Ketchum,K.A., di Francesco,V. and Beasley,E.M. Isolated human transporter proteins, nucleic acid molecules	hordata; Craniata rimates; Catarrh				124		it W00224910.	1617 bp DNA		
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VERSION
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ORGANISM RESULT 2 BC006251 LOCUS COMMENT REFERENCE ACCESSION DEFINITION AUTHORS TITLE JOURNAL REMARK NIH-MGC Project URL: http://m Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue procurement: DCTD/DTP cDNA Library Preparation: Rul Gene Colie Institute, Direct Submission Submitted (09-APR-2001) Homo Strausberg, R. Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 1468) Homo sapiens MGC BC006251.1 Homo sapiens Homo sapiens, IMAGE:3948165, Collection (MGC), tute, 31 Center D GI:13623300 1468 bp mRNA Similar to Zink transporter , mRNA, complete cds. Chordata; Primates; http://mgc Drive, Cancer Genomics Or. Rubin Craniata; Vertebrata; Catarrhini; Hominidae; Laboratory nci.nih.gov Institutes of nomics Office, Bethesda, 2 linear of clone Health, N National M PRI 12-JUL-2001 MGC:11303 Euteleostomi; Homo. 20892-2590, Mammalian ıl Cancer

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This clone was selected for full length sequencing because
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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WYVTGULVYLAVERLISGDYEIDGTWLITSGCAVAVNILITGTTLHQSGHGHBHGTTL
TILRDVILVLMEGTPKGYDFTAVRDLLLSVEGYBALHSLHIMALTVAQPVLSVHIAIA
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/clone_lib="NHH_MGC_9"
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/db_xref="taxon:9606"
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Best Local Similarity 99.9
Matches 1279; Conservative
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Sequence
AX405563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Genomics, Inc. (US)
Location/Qualifiers
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30 from Patent WO0222684.
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/db_xref="taxon:9606"
/note="Incyte ID No: 2614283CB1"
1 383 c 392 g 257 t
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99.9%;
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Pred. No. 3.7e-261;
0; Mismatches 0;
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C., Raumann, B.E.,
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VERSION KEYWORDS SOURCE

AK094027.1 GI:21753005 oligo capping; fis (full insert sequence). Homo sapiens uterus cDNA to mRNA, clone_lib:UTERU2 clone:UTERU2009904.

ACCESSION

similar to AK094027

AK094027 1818 bp Homo sapiens cDNA FLJ36708 fis, similar to ZINC TRANSPORTER 2.

PRI 15-JUL-2002

REFERENCE

ORGANISM

Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae

Hominidae;

Euteleostomi;

AUTHORS

Suzuki,O.,

Sasaki, N., Aotsuka, S.,

Shoji,T.,

RESULI AK094 LOCUS DEFIN	Ъ	Qy	망	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Дb	Qy	Db	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	Дb	Qy
ILT 4 04027 IS	1261	1347	1201	1287	1141	1227	1081	1167	1021	1107	961	1047	901	987	841	927	781	867	721	807	661	747	601	687	541	627	481	567
AK094027 1818 bp mRNA linear PRI 15- Homo sapiens cDNA FLJ36708 fis, clone UTERU2009904, moderat	GACTGCTCAGCCAGCACCA 1280	GACTGCTCAGCCAGGCACCA 1366	AGATCGAGGACTACTCGGAGGACATGAAGGACTGTCAGGCATGCCAGGGCCCCTCAGACT	AGATCGAGGACTACTCGGAGGACATGAAGGACTGTCAGGCATGCCAGGGCCCCTCAGACT	GCCAGCAGCCGCCTCCAAGGGAAGTTCCACTTCCACACCGTGACCATCC	TGCTGAAGACAGCCAGCAGCCGCCTCCAAAGGGAAGTTCCACTTCCACACCGTGACCATCC 1	GGCCCAGCCTGTTCTGTCTGTCCACATCGCCATTGCTCAGAATACAGACGCCCAGGCTG	TGGCCCAGCCTGTTCTGTCTGTCCACATCGCCATTGCTCAGAATACAGACGCCCAGGCTG 1		TGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCCTGCATATCTGGGCACTGACGG 1	TGATCCTGGTGTTGATGGAAGGGACCCCCAAGGGCGTTGACTTCACAGCTGTTCGTGATC		TCTGCACCTTCGTCTTCTCCATCCTGGTCCTGGGGACAACCTTGACCATCCTGAGAGATG 9	TCTGCACCTTCGTCTTCTCCATCCTGGTCCTGGGGGACAACCTTGACCATCCTGAGAGATG 1	GTGTCCTAGTGGCAGCCTATATTTTATACTTCAAGCCAGAATACAAGTATGTAGACCCCA 9	GTGTCCTAGTGGCAGCCTATATTTTATACTTCAAGCCAGAATACAAGTATGTAGACCCCA 9	AGAACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAGAGCATGG	AGAACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAGAGCATGG 9	GGTTGACCCTTCACCAGTCTGGCCATGGGCACAGCCACCAACCA	GGTTGACCCTTCACCAGTCTGGCCATGGGCACAGCCACGGCACCACCAACCA	TTGACGGGGGGACCATGCTGATCACGTCGGGCTGCGCTGTGGACGTCATAATGG 7	TTGACGGGGGGACCATGCTGATCACGTCGGGCTGCGCTGTGGCTGTGAACATCATAATGG 8	TCGTGACGGGGGTACTGGTGTACCTGGCTGTGGAGCGGCTGATCTCTGGGGACTATGAAA 6	TCGTGACGGGGGTACTGGTGCACCTGGCTGTGGAGCGGCTGATCTCTGGGGACTATGAAA 7	ACTITIGGCIGGCAGAGAGCTGAGATCTIGGGAGCCCTGGTCTCTGTACTGTCCATCTGGG	ACTITIGGCTGGCAGAGAGCTGAGATCTTGGGAGCCCTGGTCTCTGTACTGTCCATCTGGG 6	GCATGCTCATCAGCCTCTTCTCCCCTCTGGATGTCCTCCCGGCCAGCCA	GCATGCTCATCAGCCTCTTCTCCCTCTGGATGTCCTCCCGGCCAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:s1-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center of Seconomy, Takional Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB, RAB; annotation: HRI and RAB.
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Isogai,T. and Yamamoto,J.
Direct Submission
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/clone_lib="UTERU2"
/note="cloning vector:
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shqc.stanford.edu
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
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Mus musculus, clone IMAGE:4239648,
BC013478
                                                                                                                                                                                  Series: IRAK Plate: 25 Row: h Column: 6
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 25 Row: h Column: 6
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Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                /tissue_type="Kidney, normal.
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
                                                                          /map="FVB/N"
/clone="IMAGE:4239648"
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                                                                                                                                                                      Location/Qualifiers
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Submitted (07-MAR-1996) Richard D. Palmiter,
Institute, University of Washington, Health
Box 357370, Seattle, WA 98195-7370, USA
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                          Conservative
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                                                                                                                                                                                          MLITSGCAVAVNIIMGLALHQSGHGHSHGHSHEDSSQQQQNPSVRAAFIHVVGDLLQS
VGVLVAAYIIYEKPEYKYVDPICTFLESILVLGTTLTILRDVILVLMEGTPKGVDFTT
VKNLLLSVDGVEALHSLHIMALTVAQPVLSVHIAIAQNVDAQAVLKVARDRLQGKFNF
HTMTIQLESYSEDMKSCQECQGPSE"
1 411 c 426 g 369 t
                                                                                                                                                                                                                                                                                /transl_except*(pos:52..54,aa:Met)
/product="zinc transporter ZnT-2"
/protein_id-"AnB02775.1"
/db_xref="GI:1256378"
/translation="MASRSFFGALWKSEASRIPPVNLPSVELAVQSNHYCHAQKDSGS
HPNSEKQPARKKIYNASAICLVFMIGEIIGGYLAQSLAIMTDAAHLLTDFASMLISLF
SLWYSSRPATKTMNFGWQRAEILGALLSVLSIWVVTGYLVLLAVQRLISGDYEIKGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Sprague Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ZnT-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="2nT-2"
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                                                                                                                        45.4%;
78.5%;
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                                                                                                      Score 734.4; DB 10;
Pred. No. 7.6e-147;
0; Mismatches 226;
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PRI 01-AUG-2002 weakly similar

Suzuki,Y.,

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GAGAACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAGAGCATG
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                       TGACTGCTCAGCCAGGCACCAACT
                                                                                                      CAGATCGAGGACTACTCGGAGGACATGAAGGACTGTCAGGCATGCCAGGGCCCCTCAGAC
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ACTTCACAGCTGTTCGTGATCTGCTGCTGCTGGTGGAGGGGGTAGAAGCCCTGCACAGCC
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Isogai, T. and Otsuki, T.
Direct Submission
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- 8 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
Instructive of Tuburo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk. Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishi,S., Kawai,Y., Salto,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayana, Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayana, Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayana, Nakamoro DNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence). Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1clone:PLACE1002500.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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to Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="placenta"
/clone_lib="PLACE1"
/note="cloning vector: |
663 c 647 g 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    37.2%;
100.0%;
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Nishikawa,T., Nagal,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
NEDO human cDNA sequencing project
Unpublished
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                                                                                                                                                                                                      Unpublished

2 (bases 1 to 1440)

1 sogai, T. and Otsuki, T.

Direct Submission

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 152-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1 clone:PLACE1002782.
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                                                                                                                                                                                            University of Tokyo.
                  /db_xref="taxon:9606"
/clone="pLACE1002782"
/tissue_type="placenta"
/clone_lib="pLACE1"
/note="cloning vector: pl
a 420 c 412 g 310
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Eutheria;
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Primates;
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                                                                                                                                                              Wei,M.H., Ketchum,K.A., di Francesco
Isolated human transporter proteins,
encoding them, and uses thereof
Patent: WO 0224910-A 3 28-MAR-2002;
PE Corporation (NY) (US)
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Sequence 3 from Patent W00224910.
AX411375 AX411375.1 GI:21444025
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                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
3041 c 3200 g 244
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100.0%; Pred. No. 3.8e-101;
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                                                                                                                                                                                                                                                                                      Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, curscappor. The Transfer on the WORMERP.
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                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 constructed by the Sanger Centre Chromosome 1 Mapp: Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 2001 this sequence version replaced gi:16605685.
During sequence assembly data is compared from overlapping clones.
This sequence is the entire insert of clone RP11-96L14 The true left end of clone RP11-231P20 is at 72881 in this sequence. The true right end of clone RP11-111D20 is at 72886 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                         RP11-96L14 is from the library RPCI-11.1 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                       SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                 VECTOR: pBACe3.6
                                                                                     //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (28-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
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U76007.1
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Palmiter,R.D., Cole,T.B., Quaife,C.J. and Findley,S.D.
ZnT-3, a putative transporter of zinc into synaptic ve
Proc. Natl. Acad. Sci. U.S.A. (1996) In press
2 (bases 1 to 1952)
Palmiter,R.D., Cole,T.B., Quaife,C.J. and Findley,S.D.
                                                                                                                                                  Submitted (23-OCT-1996) Howard Hughes Medical Institute, of Washington, Box 357370, Seattle, WA 98195, USA
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Mus musculus zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                     /organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="taxon:9606"
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GAGATGTTCTCCTTGTCCTCATGGAAGGCGCCCCTCGGAGTGTGGAATTTGAACCCGTAA 1044
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EGHGYPMSLGNTSVRAAFVHVLGDLLQSFGVLAASILIYFKPQYKVADPISTFLFSIC
ALGSTAPTLRDVLLVLMEGAPRSVEFEPVRDTLLSVPGVRATHDLHLMALTLIYHVAS
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MTDAAHLLADIGSMLASLFSLWLSTRPATRTWTFGWHRSETLGALASVVSLWIVTGIL
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/function="zinc transporter"
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Palmiter, R.D., Cole, T.B., Quaife, C.J. and Findley, S.D. 2nT-3, a putative transporter of zinc into synaptic ve Proc. Natl. Acad. Sci. U.S.A. (1996) In press
2 (bases 1 to 2000)
Palmiter, R.D., Cole, T.B., Quaife, C.J. and Findley, S.D.
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/db_xref="01:1763376"
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/translation="mepspaagglettrlvsprdrggaggslrlkslftepseplpee
/translation="mepspaagglettrlysprdrgagaggslrlkslftepseplpee
SKPVEMPFHKCHRDPLPPPGLTPERLHARRQLYAACAVCFVFMAGEVVGGYLAHSLAI
MTDAAHLLADVGSMMGSLFSLWLSTRPATRTMTFGWHRSETLGALASVVSLWMVTGIL
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BC028358.1
                                                                  BC028358 2101 bp mRNA linear PRI 25 Homo sapiens, solute carrier family 30 (zinc transporter), 3, clone MCC:26355 IMAGE:4837595, mRNA, complete cds.
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 TGTGGGCAGCATGATGGGCAGCCTCTTCTCCCCTCTGGCTCTCCACCCGTCCAGCCACCCG
                   ACGGAGGCAGCTATATGCTGCCCTGTGCCGTTTGCTTTGTCTTCATGGCTGGGGAGGTGGT
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 450804:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NH
CDNA Library Preparation: (RIKEN)
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
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Gene Collection (MGC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
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contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Contact: MGC help desk
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/db_xref="taxon:9606"
/clone="MGC:26355 IMAGE:4837595"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
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/tdb_xref="G1:20306868"
/translation="merspaagglettruvsprdrggacgslrlksletepseplpee
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Lylafvellhadvcsmmgslfslwistrpatrollumafvlhqagpphshegsgabyapte
Lylafvelthsdytleggamlltarslavcanllliyfkpgykaadplistflfsic
egpeeplplgntsvraafyhvlgdllqsfgylaasilliyfkpgykaadplistflfsic
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AHLAIDSTADÞEAVLAEASSRLYSRFGFSSCTLQVEQYQÞEMAQCLRCQEÞÞQA"
a 692 c 627 g 467 t
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Sequence 57
AX061210
AX061210.1
        Human transport proteins
Patent: WO 0078953-A 57 28-DEC-2000;
Incyte Genomics, Inc. (Te)
                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; I (bases 1 to 2823)

1 (bases 1, Yang, J., Yue, H., Hillm
                                                     Burford, N., Patterson, C.
                                                                                                                                   Homo sapiens
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Genomics, Inc. (US)
Location/Qualifiers
                                                                 g,J., Yue,H.,
Baughn,M.R.,
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4	590	36.5	732	22	AAH07440	Human cDNA clone
₅	521	32.2	783	22	AAH07460	Human cDNA clone
σ	521	32.2	1440	22	AAH16516	Human cDNA sequen
7	363.6	22.5	11101	24	ABN83947	Human transporter
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ALIGNMENTS

RESULT 1	LT 1
ABN83946	3946
IJ	ABN83946 standard; cDNA; 1617 BP.
×	•
AC	ABN83946;
XX	
PΤ	02-OCT-2002 (first entry)
X	
DE	Human transporter protein encoding cDNA.

Human; transporter protein; zinc transporter; pharmacogenomic analysis; diagnosis; drug screening; gene therapy; kidney; testis; heart; placenta; small intestine; liver; chromosome 1; gene; ss. Homo sapiens

XXXXXXXX

PΑ	XX	PR	PR	XX	ΡF	×	ρD	XX	ΡN	X	FΤ	FΤ	FΤ	FH
(PEKE) PE CORP NY.		19-OCT-2000;	20-SEP-2000;		20-SEP-2001;		28-MAR-2002.		WO200224910-A2.				CDS	Key
ORP NY.		19-OCT-2000; 2000US-0691219.	2000US-234160P.	•	20-SEP-2001; 2001WO-US29218.				42.		<pre>/product= "transporter protein"</pre>	/*tag= a	2301348	Location/Qualifiers

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Best Local Similarity
Matches 1617; Conserv
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ACCCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TCCCAGCCTCCCATCTGACTACAGCCAGGGTGGGGACTCAGCGGGTATAAAGCTAGTGTG 15 	AGCTGTGTTATAAACCAGGTCCCCCTCCTGACCTCTGCCCACTCCAGGAATGGAGCTCT 15 	AGGACCTGCAGGTGGCTGGACTGAGTGTCCCCCAGGCCCAGGCCAGGACTTTGCCTACCCC 14	TCAGGCATGCCAGGGCCCCTCAGACTGACTGCTCAGCCAGGCACCAACTGGGGCATGAAC 13	GTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGACATGAAGGACTG 13 	TGCTCAGAATACAGACGCCCAGGCTGTGCTGAAGACAGCCAGC	CAGCCTGCATATCTGGGCACTGACGGTGGCCCAGCCTGTTCTGTCTG	CGTTGACTTCACAGCTGTTCGTGATCTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCA 11 	GACAACCTTGACCATCCTGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCAAGGG 1	GCCAGAATACAAGTATGTAGACCCCATCTGCACCTTCGTCTTCTCCCATCCTGGTCCTGGG 1	GATCGGCGACTTTATGCAGAGCATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTCAA 9 	CCACGGCACCACCAGCAGGAGGAGGAGAACCCCAGCGTCCGAGCTGCCTTCATCCATGT 9	GGTTGACCCTTCACCAGTCTGGCCATGGGCACAG 8	CGGGCTG 7	CCTGGTCTCTGTACTGTCCATCTGGGTCGTGACCGGGGTACTGGTGTACCTGGCTGTGGA 7	CTCCCGGCCÄGCCACCAAGACCATGAACTTTGGCTGGCAGAGAGCTGAGATCTTGGGAGC 6
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RESULT 2
AAD36301
ID AAD36301 standard;

1280 BP

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The invention relates to human transporters and ion channels (TRICH) CC and their corresponding nucleic acid sequences. TRICH is useful for Screening an agonist/antagonist that modulates its activity. TRICH is CC useful as an immunogen for preparing antibodies which are useful for CC diagnosing a condition of disease associated with its expression in a Subject, and for detecting and purifying it from a sample. TRICH DNA CC is useful as probe or a primer for assessing toxicity of a test CC compound. Composition comprising TRICH or its agonist is useful for treating a disease or condition associated with decreased expression CC of functional TRICH and composition comprising TRICH antagonist is useful for treating a disease or condition associated with TRICH STRICH Sequence is used in the diagnosis and CC treatment of transport disease or condition associated with TRICH Alzheimer's disease; neurological disorder e.g. diabetes mellitus, angina, Alzheimer's disease; neurological disorder e.g. epilepsy, stroke, CC Huntington's disease; neurological disorder e.g. epilepsy, stroke, CC immunological disorder e.g. acquired immunodeficiency syndrome (AIDS), allergies, atherosclerosis; and cell proliferative disorders e.g. cirrhosis, hepatitis, psoriasis and cancers. TRICH DNA is used in the manised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee EA, Yue H, Lal PG,
Sanjanwala MS, Yao MG, I
Policky JL, Elliott VS,
Hafalla AJA, Nguyen DB,
Reddy RM, Burford N.
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22-SEP-2000;
29-SEP-2000;
05-OCT-2000;
13-OCT-2000;
18-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                        Claim
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antiinflammatory;
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2000US-234842P.
2000US-236882P.
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2000US-240540P.
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Arvizu C, I
Xu Y, Lu D
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Thornton M, Gandhi AI
Raumann BE, Bruns CM,
DAM, Ison CH, Griffin
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                           GTGTCCTAGTGGCAGCCTATATTTATACTTCAAGCCAGAATACAAGTATGTAGACCCCA
                                                                                     CCGCAGGAGCCGGGCCGGAGTGAGCGCACCTCGCGGGG-CCCTCGGGGCAGGTGGGTGAG
                                                       TTGACGGGGGGACCATGCTGATCACGTCGGGCTGCGCTGTGGCTGTGAACATCATAATGG
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                                                                                                                                                TCGTGACGGGGGTACTGGTGTACCTGGCTGTGGAGCGGCTGATCTCTGGGGGACTATGAAA
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                                                                                                                                                                                    ACTTTGGCTGGCAGAGAGCTGAGATCTTGGGAGCCCTGGTCTCTGTACTGTCCATCTGGG
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99.9%;
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Pred. No. 7.2e-
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as years a sequence complementary to the complementary to the
                                                                                                                                                                                                                                                                                                                                                                                       Ota T,
Ishii :
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                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama
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; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                for synthesizing cDNAs defined in
                                                                                                                                                                                            ID 15542;
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T, Wakama
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Wakamatsu
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abnormality of the proteins encoded by the
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A, Nagai K,
                                                                                                                                                                                               ROM;
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C, Otsuki
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301

ACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGGAGGACATGAAGGACTGTCAGG AGAATACAGACGCCCAGGCTGTGCTGAAGACAGCCAGCAGCAGCCGCCTCCAAGGGAAGTTCC 1326

361

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1266 241

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181

1206

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CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers ere seful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNAs sequences; AAAB92446 to CC CAAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                            Best
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ACTICACAGCTGTTCGTGATCTGCTGCTGCTGGTGGAGGGGGTAGAAGCCCTGCACAGCC 1145
                                                                                                                                                    CCTTGACCATCCTGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCAAGGGCGTTG
                                                                                                                                                                      CCTTGACCATCCTGAGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCAAGGGCCTTG
                                                                 ACTTCACAGCTGTTCGTGATCTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCC
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nilarity 100.0%;
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RESULT
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DT 26 B AAH07440; 26-JUN-2001 AAH07440 601 G 601 standard; (first entry) 732

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TGTTATAAACCAGGTCCCCCTCCTGACCTCTGCCCACTCCAGGAATGGAGCTCTTCCCA

TGTTATAAACCAGGTCCCCCTCCTGACCTCTGCCCCCACTCCAGGAATGGAGCTCTTCCCA

CATGCCAGGGCCCCTCAGACTGACTGCTCAGCCAGGCACCAACTGGGGCATGAACAGGAC CATGCCAGGGCCCCTCAGACTGACTGCTCAGCCAGCCACCCAACTGGGGCATGAACAGGAC

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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                      the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
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T, Wakamatsu
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No. 2.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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, Sugiyama
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n T, Wakama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGCCCAGCCTGTTCTGTCTGTCCACATCGCCATTGCTCAGAATACAGACGCCCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCCTGCATATCTGGGCACTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 521; I
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3e-97;
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RESULT 6
AAH16516
ID AAH1
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AC AAH1
XX

AAH16516 standard;

cDNA;

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1166

GTGGCCCAGCCTGTTCTGTCTGTCCACATCGCCATTGCTCAGAATACAGACGCCCAGGCT

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AAH16516;

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                                                                                                                                                                                                                                        CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which complises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of a noligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary com
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                          Matches 521;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                      1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2001
                                                                                                                                                                                                                                      Sequence 1440
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61
                                                                                                                                                                             Local Similarity
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                                      CTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCCTGCATATCTGGGCACTGACG
                                                                             GTGATCCTGGTGTTGATGGAAGGGACCCCCCAAGGGCGTTGACTTCACAGCTGTTCGTGAT
                                                                                                   GTGATCCTGGTGTTGATGGAAGGGACCCCCAAGGGCGTTGACTTCACAGCTGTTCGTGAT 1105
  CTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCCTGCATATCTGGGCACTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 15557; 2537pp + CD ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                        BP;
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                                                                                                                                                        0;
                                                                                                                                                        Score 521; DB; Pred. No. 3.9; Mismatches
                                                                                                                                                                                                                                        C; 412
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ı A, Nagai K
                                                                                                                                                                                                                                      G;
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transporter protein; zinc transporter; pharmacogenomic analysis; diagnosis; drug screening; gene therapy; kidney; testis; heart; placent small intestine; liver; chromosome 1; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transporter protein encoding genomic DNA
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                                                                                                                                                                                                                                                                                                intron
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/number= 2
3736..3882
                                     /number= 4
4784..5472
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/number= 1
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/note= "contains 7 introns"
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2284..8840
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exon
                                                                                                          Claim 4(b); Fig 3; 75pp; English.
                                                                                                                                       WPI; 2002-404954/43.
P-PSDB; ABB83084.
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19-OCT-2000; 2000US-0691219
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                                                                                                  The invention relates to an isolated human transporter protein
                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                       20-SEP-2001;
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/*tag= j
/number= 5
5633..6375
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8695..8838
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/number= 6
8089..8223
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                                                                                                                                                      Beasley
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Novel human transporter proteins, related to zinc transporter subfamily, useful as model for developing human therapeutic targets and serves as target for human therapeutics -

condition mediated by human transporter protein. The proteins also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, inappropriate or unwanted expression of the protein. The nucleic acids are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention has been found to be expressed in humans in the kidney, testis, heart, placenta, small intestine and liver. The gene has been localised to human chromosome 1. The current sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding recents of the sequence represents the human transporter protein encoding the transporter testification to the sequence represents the human transporter protein encoding the transporter testification to the sequence represents the human transporter testification that the sequence represents the human transporter testification to the sequence represents the sequence represents the human transporter testification to the sequence represents the sequence represents the human transporter testification to the sequence represents the sequence represents the se protein encoding genomic DNA.

Note: This sequence contains 6 single nucleotide polymorphisms (SNP's), but information given in the specification is insufficient to determine their locations within this sequence (see ABN83948-ABN83953 for specification). related to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease regions). transporter that specific is

Sequence 11101 вP; 2403 A; 3041 C; 3200 ç, 2448 7 9 other;

Query Match Best Local S Matches 366 Similarity Conservative 22.5%; 98.9%; 0; Score 363.6; Pred. No. 9.9 ed. No. 9.9e Mismatches .9e-65; DB 24; Indels Length 11101; 0; Gaps

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11-JAN-2001;
26-JAN-2001;
09-MAR-2001;
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13-OCT-2000;
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                  2000US-233382P
2000US-2334012P
2000US-233521P
2000US-233522P
2000US-233801P
2000US-233890P
2000US-2438398P
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Tchernev VT, M
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Gunther E, Elle
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, Malyankar UM, Shenoy S,
M, Burgess CE, Smithson G,
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S, Tchernev VT,
n G, Millet I, F
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New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumours, lung disorders, haematopoietic disorders, autoimmune diseases and immune disorders

Claim 9; Page 21; 210pp; English.

a vector comprising the nucleic acid; a cell comprising the vector; an anti-Novx antibody; and identifying agents that modulate the expression or activity of Novx. Novx the nucleic acid, antibody and modulators are useful in the diagnosis, treatment or prevention of developmental disorders, endocrine disorders, vascular disorders, infectious disease, anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, and amyotropic lateral sclerosis, acute brain injury (e.g. stroke, head injury and cerebral palsy), central nervous system disorders (e.g. depression, epilepsy and schizophrenia), lung disorders, reproductive disorders, disorders affecting carbohydrate metabolism (e.g. galactosaemia and hereditary fructose intolerance), tissue disorders (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness ar pick's disease), disorders linked to abnormal angiogenesis, asthma, azoospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, X-linked severe combined immunodeficiency, seizure migraines, inflammation, autoimmune disorders, disorders affecting sleep, appetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasitic infections, hyper or hypothyroidism, endometriosis, fertility, hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-lin mental retardation, psychotic and neurological disorders and neuronal degeneration. NOV5a, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant. Also included are a nucleic acid encoding a NOVX protein or variant; invention NOV1b, The relates to an isolated NOVX polypeptide selected from NOV1ac, NOV2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4a, NOV4b, present sequence encodes a NOVX protein seizures x-linked and

Sequence 1318 BP; 337 A; 329 C; 308 G; 344 T; 0 other;

Query Match Best Local Matches

574;

Conservative

0 Pred. Score 309.6;

Mismatches No.

409; 24;

9;

Gaps

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Length 1318;

Similarity

19.1%; 57.9%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; gene; NOVX; developmental disorder; endocrine disorder;
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(e.g. depression, epilepsy and schizophrenia), lung disorders, reproductive disorders, disorders affecting carbohydrate metabolism (e.galactosaemia and hereditary fructose intolerance), tissue disorders (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and pick's disease), disorders linked to abnormal angiogenesis, asthma, azoospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, x-linked severe combined immunodeficiency, seizures, migraines, inflammation, autoimmune disorders, disorders affecting sleep appetite, thermoregulation, pain, perception, hormone secretion and several behaviour immune disorders has a servant serval s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOV1a, NOV1b, NOV1ac, NOV2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4a, NOV4b, NOV5b, NOV5b, NOV4a, NOV5b, N
                                                                                                                                                                                                            sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasi infections, hyper- or hypo-thyroidism, endometriosis, fertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious disease, anorexia, cancer, neurodegenerative disorders (e.g. Alzhelmer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis and amyotropic lateral sclerosis), acute brain injury (e.g. stroke, head injury and cerebral palsy), central nervous system disorders
                                                                                                                                           hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, syndrome, rheumatoid arthritis, Grave's disease, wound healing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 19-20; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumours, lung disorders, haematopoletic disorders, autoimmune diseases and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated NOVX polypeptide selected from NOVIa, NOVIb, NOVIac, NOV2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4a, NOV4b,
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Patturajan M,
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                                                                                                            mental retardation, psychotic and neurological disorders and
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13-OCT-2000;
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2000US-233521P
2000US-233522P
2000US-233801P
2000US-23380P
2000US-23838P
2000US-240284P
2000US-240284P
2000US-24074P
2001US-260973P
2001US-264274P
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                                                                     sequence encodes
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                                                                     a NOVX protein
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                                                                      AAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGACATGAAGGAC
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                        TGTCAGGCATGCCAGGGCCCCTCAGACTGACT
                                                                                                             ACAGCAGCCAGCTGGGACAGCCAAGTGGTTCGGAGAGAATTGCTAAAGCCCCTTAGCAAA
                                                                                                                                        CACAGCCTGCACATCTGGTCTCTAACAATGAATCAAGTAATTCTCTCAGCTCATGTTGCT
                                                                                                                                                                                                                          AAGCCAGAGTATAAAATAGCCGACCCAATCTGCACATTCATCTTTTCCATCCTGGTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGCAGTGGCGGCCAACATTGTACTAACTGTGGTTTTTGCACCAGAGATGCCTTGGCCAC
                                                      {	t AGCTTTACGATGCACTCACTCACCATTCAGATGGAATCTCCAGTTGACCAGGACCCCGAC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCACGGCACCAACCAGCAGGAGGAGAACCCCCAGCGTCCGAGCTGCCTTCATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CAAGGAAGTACAAGCCAATGCCAGCGTCAGAGCTGCTTTTGTGCAT
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RESULT 10 ABK88011

disorders, disorders of the small intestine, disorders of metal ion imbalance, protein trafficking disorders and disorders associated w. bone metabolism. The sequences of the invention are also useful for screening assays, predictive medicine (e.g., diagnostic associated w.

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or 84234 podiagnosing
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14-NOV-2000;
30-NOV-2000;
30-NOV-2000;
30-NOV-2000;
                                                      an inability to clear infections (e.g., viral or bacterial infections), as well as disorders related to abnormal cellular proliferation or differentiation, e.g., leukaemia. They may also be used to control disorders of metabolic imbalance (e.g., disorders of lipopolysaccharide biosynthesis or glycogen synthesis) immunological disorders, cardiovascular disorders, neurological disorders, cellular proliferation and/or differentiation disorders, e.g., cancer, cell motility and adhesion disorders differentiative disorders, red blood cell disorders, viral diseases, neurological disorders, kidney disorders, pain or metabolic disorders, liver disorders, kidney disorders, disorders, disorders, kidney
                                                                                                                                                                                                                                                                                           This invention relates to the DNA and protein sequences of novel isolated 47476, 67210, 49875, 48842, 33201, 83378, 84233, 64708, 85041 or 84234 proteins. The method of the invention is useful for treating a disorder characterised by aberrant activity of 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 85041 or 84334-expressing cell in a 46842, 33201, 83378, 84233, 64708, 85041 or 84334-expressing cell in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84233; metal transporter; human; ss; gene; infection; haematopoeitic disorder; blood clotting disorder; cancer; autoimmune disorder; leukaemia; immunological disorder; cardiovascular disorder; neurological disorder; cellular red blood cell disorder; viral disease; neurological disorder
                                                                                                                                                                                                                          subject. The protein molecules can act as novel diagnostic targets and therapeutic agents for controlling aberrant or deficient signal transduction resulting, in e.g., haematopoeitic disorders, including blood clotting disorders, autoimmune disorders, or disorders related blood clotting disorders, autoimmune disorders, or disorders related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 236-237;
                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
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)B; AAU99907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-248362P.
2000US-248365P.
2000US-250077P.
2000US-250176P.
2000US-250327P.
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/note= "This sequence is specifically
claimed in claim 1 of the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            46842, 33201, 83378, 84233, 64708, 8 as reagents or targets for treating liver, kidney, or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2165 BP;
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AAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGACATGAAGGAC
                                                                                                                                                             GGGACAACCTTGACCATCCTGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                               AAGCCAGAATACAAGTATGTAGACCCCCATCTGCACCTTCGTCTTCTCCCATCCTGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGATCGGCGACTTTATGCAGAGCATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTC
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                                                                                                                                                                                                                  GGCGTTGACTTCACAGCTGTTCGTGATCTGCTGCTGGTGGAGGGGGGGTAGAAGCCCTG
                                                                                                                                                                                                                                                                                             GCCAGCACCATCACTATCTTAAAGGACTTCTCCATCTTACTCATGGAAGGTGTGCCAAAG
                                                                                                                                                                                                                                                                                                                                                                           AAGCCAGAGTATAAAATAGCCGACCCAATCTGCACATTCATCTTTTCCATCCTGGTCTTG
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                                                           ACAGCAGCCAGCCGGGACAGCCAAGTGGTTCGGAGAGAATTGCTAAAGCCCCTTAGCAAA
                                                                                               CACAGCCTGCACATCTGGTCTCTAACAATGAATCAAGTAATTCTCTCAGCTCATGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATCA-----CAAGGAAGTACAAGCCAATGCCAGCGTCAGAGCTGCTTTTGTGCAT
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57.9%;
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No. 7.2
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GAGCTGGAGTCAGGAGGCATGTACCACTGCCACAGTGGCTCCAAGCCCACAGAAAAAGGGG GAGCTGGCCTGCCCAGAGCAACCATCACTGCCCATGCTCAGAAGGGTCCTGACAGTCACTGT 418 Query Match Best Local S Matches 574

Similarity

19.1**%**; 57.9**%**;

0;

Pred. No. 7.3); Mismatches Score

9

Gaps

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309.6; DB 2 No. 7.3e-54;

DB 23; T; 7 other;

Sequence

BP;

692 A; 506

C;

491 G;

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RESULT 11
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XX ABV23919
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XX ABV23
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                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 4416-4417; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlegel
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13-DEC-2000;
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09-JUN-2000;
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16-MAR-2000;
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GCAGCACACCTGCTCACTGACTTTGCCAGCATGCTCATCAGCCTCTTCTCCCCTCTGGATG

GCTGCCCACCTCTTAATTGACCTGACCAGTTTCCTGCTCAGTCTCTTCTCCCTGTGGTTG

TTCATGATTGCAGAGGTCGTGGGTGGGCACATTGCTGGGAGTCTTGCTGTTGTCACAGAT

677

GACCCCAAGAAGGGGAAGGCCCAGCGCAGCTGTATGTAGCCTCTGCCATCTGCCTGTTG GAGCTGGAGTCAGGAGGCATGTACCACTGCCACAGTGGCTCCAAGCCCCACAGAAAAGGGG

478

557

 ${\tt GCGAATGAGTACGCCTATGCCAAGTGGAAACTCTGTTCTGCTTCAGCAATATGCTTCATT}$

539 618 Query Match 19.1 Best Local Similarity 57.9 Matches 574; Conservative

19.1%; 57.9%;

0;

Score 309.6; DB 2 Pred. No. 7.3e-54; 0; Mismatches 409

Indels Length

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DB 23; 409;

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GAGCTGGCTGCCCAGAGCAACCATCACTGCCATGCTCAGAAGGGTCCTGACAGTCACTGT 418

479 558

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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                      (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate pharmacogenomic
 Sequence
                                                                                                                                      cancer in a patient;
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692 A; 506 C; 491 G;
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gene; ss.
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                                                                                                                                                                                                                                                                            Human; transport protein; TPPT; transport disorder; metabolic neurological disorder; cardiovascular disorder; reproductive of
     17-JUN-1999;
                                                 16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                   Human transport protein TPPT-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF27714 standard;
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18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide with a human transport protein sequence for the diagnosis, prevention and treatment of disorders assowith the immune, reproductive and cardiovascular systems -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 148-149; 165pp; English.
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P-PSDB; AAB60094.
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                                                          GTGATCGGCGACTTTATGCAGAGCATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTC
                                                                                                                 AGCCACGGCACCAACCAGCAGGAGGAGGAGCCCCAGCGTCCGAGCTGCCTTCATCCAT
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99US-0149357.
99US-0162287.
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14-NOV-2000;
15-MAY-2001;
The invention relates to human pancreatic tumour polypeptides and nucleic acid molecules encoding such polypeptides. The invention also relates to compositions and methods for the diagnosis, prevention and therapy of cancer, particularly pancreatic cancer
                                                                                               WPI;
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                                           Claim 1;
                                                            Pancreatic prevention
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                                                        GCCAGCACCATCACTATCTTAAAGGACTTCTCCATCTTACTCATGGAAGGTGTGCCAAAG
                                                                                                                                                                                               GGGACAACCTTGACCATCCTGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCCAAG
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AGCTTTACGATGCACTCACTCACCATTCAGATGGAATCTCCAGTTGACCAGGACCCCGAC
                     AAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGACATGAAGGAC
                                          ACAGCAGCCAGCCGGGACAGCCAAGTGGTTCGGAGAGAAATTGCTAAAGCCCCTTAGCAAA
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No. 7.7e-54;
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20-SEP-2000;
06-OCT-2000;
13-OCT-2000;
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15-SEP-2000;
15-SEP-2000;
18-SEP-2000;
          The invention relates to an isolated NOVX polypeptide selected from MOV1a, NOV1b, NOV1ac, NOV2a, NOV2c, NOV3a, NOV3b, NOV3b, NOV4a, NOV4b, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant Also included are a nucleic acid encoding a NOVX protein or variant; a vector comprising the nucleic acid; a cell comprising the vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular disorder; infectious disease; anorexia; cancer; stroke; neurodegenerative disorder; Alzheimer's disease; acute brain injury; central nervous system disorder; depression; lung disorder; reproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1390
                                                                                                                     New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumours, lun haematopoietic disorders, autoimmune diseases and immune d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK71913 standard;
                                                                                                                                                                                                                                      Tchernev VT,
Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2000;
19-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding Zinc transporter-like protein NOV2b
                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2000;
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anti-NOVX antibody;
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                                                                                                                                                                                  ABG60225.
                                                                                            Page
                                                                                                                                                                                                                        Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; NOVX; developmental disorder; endocrine disorder;
                                                                                                                                                                                                                     Syptek KA, Taupier RJ, Vei, Malyankar UM, Shenoy S, M, Burgess CE, Smithson G, unther E, Ellerman K;
                                                                                                                                                                                                                                                                                                                     2000US-23352P.

2000US-233801P.

2000US-233960P.

2000US-23398P.

2000US-240284P.

2000US-240498P.

2000US-260973P.

2001US-264274P.

2001US-274862P.
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2000US-232679P.
2000US-233382P.
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2000US-233521P.
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and
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identifying agents that modulate
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                                                                                                                                                                                                                                                               Vernet CAM,
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                                                                                                                        tumours, lung disord and immune disorders
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                                                                                                                                                                                                                                                               Colman SD,
                                                                                                                                                                                                                                                  Padigaru
                                       or variant.
                                                                                                                           disorders,
                                                                                                                                                                                                                                                               Gorman
                                                     NOV4b,
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galactosaemia and hereditary fructose intolerance), tissue disorders (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and Pick's disease), disorders linked to abnormal angiogenesis, asthma, azoospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, X-linked severe combined immunodeficiency, seizures, migraines, inflammation, autoimmune disorders, disorders affecting sleep, appetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasitic typertons or hypothyrodism, endmetriosis, fertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression or activity of NOVX. NOVX, the nucleic acid, antibody and modulators are useful in the diagnosis, treatment or prevention of developmental disorders, endocrine disorders, vascular disorders (e.g. infectious disease, anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis and amyotropic lateral sclerosis), acute brain injury (e.g.
                                                                                                                        hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reproductive disorders, disorders affecting carbohydrate metabolism (e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stroke, head injury and cerebral palsy), central nervous system disorders
                                                            degeneration. The present sequence encodes a NOVX protein.
                                                                                             mental retardation, psychotic and neurological disorders and neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          depression, epilepsy and schizophrenia), lung disorders
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Sequence 1623 BP; 437 A; 380 C; 358 G; 448 T; 0 other;

Query Match Best Local Sir Matches 549;

Similarity

16.6%; 55.2%;

Score 267.8; DB Pred. No. 2.4e-45 Mismatches

2.4e-45; nes 437; 24;

Indels Length

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TTATACTTCAAGCCAGAATACAAGTATGTAGACCCCATCTGCACCTTCGTCTTCTCCATC

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1021 ATCTACTTTAAGCCAGAGTATAAAATAGCCGACCCAATCTGCACATTCATCTTTTCCATC
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Search completed: March 29, 2003, 17:18:37 Job time: 493.122 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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1617
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	1	Length	- BB	DB ID	Description
1				9	AU135613	AU135613 AU135613
2	565.6	35.0	1627	14	BM918933	BM918933 AGENCOURT
w	521	32.2	783	9	AU135737	AU135737 AU135737
4	510.8	31.6	931	14	BQ219887	BQ219887 AGENCOURT
υī	410.8	25.4	828	12	BE746716	BE746716 601579148
ი ი	389.2	24.1	394	12	BF509598	BF509598 UI-H-BI4-

BJ524737 BJ013993 BJ013993 BJ028152 BM386576 UI-R-CN1- BJ062415 BJ062415 BF524462 UI-R-C3-t	13 BJ062415 12 BF524462				
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ВJ524737 ВJ524737	вJ01399		•	189	39
	вJ52473		•	8	38
вJ056206 вJ056206	вJ05620			190.2	37
BJ038722 BJ038722	вJ03872			92	36
AW147502 da03g09.y	AW14750		•	_	35
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BO417284 1k36b01.y	BQ41728			207.4	32
BM554028 AGENCOURT	BM55402			2	<u>ω</u>
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AL792775 AL792775					29
AL799760 AL799760	AL799760		•	7	28
ВJ042222 ВJ042222				H	27
AL782327 AL782327	AL782327		•	211.4	26
BE014623 126423 MA				1	25
BM925306 AGENCOURT	BM92530		•	K 1	24
AL641096 AL641096				3	23
AL782009 AL782009	AL782009			222.2	22
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AL792631 AL792631	AL792631			2	20
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AL631343 AL631343			•	240	17
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AL651875 AL651875	AL651875			71	12
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BB620842 BB620842	BB62084			9	10
AI925963 wh12g11.x				36	9
AU138346 AU138346	AU138346			325.4	8
BE741089 601594088				73	7

ALIGNMENTS

	TITLE JOURNAL COMMENT	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AU135613 LOCUS DEFINITION
Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.	HRI human cDNA project Unpublished (2000) Contact: Takao Isogai	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 732) Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.	sequence. AU135613 AU135613.1 GI:10996152 EST. Homo sapiens	AU135613 PLACE1 Homo sapiens cDNA clone PLACE1002500 5', mRNA

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AGENCOURT_6653483 NIH_MGC_120
5', mRNA sequence.
BM918933
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pME18SFL3"
226 c 200 g 146
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/db_xref="taxon:9606"
/clone="PLACE1002500"
/clone_lib="PLACE1"
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Pred. No. 5.6e-81;
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Tissue Procurement: Life Technologies,
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/clone="IMAGE:5748088"
/clone_lib="NIH_MGC_120"
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HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

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Contact: Takao Isogai
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/db_xref="taxon:9606"
/clone="pLACE1002782"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
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Nakamura,Y., Nac
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· 	Qy 1346	
		TCCTGACCTCTGCCCCACTCCAGGAATGGAGCTCTTCCCAGCCTCCCATCTGACTACAGC
	Qy 1526 Db 481	CAGGGTGGGACTCAGCGGGTATAAAGCTAGTGTGACCCTG 1566
	RESULT 4 BQ219887 LOCUS DEFINITION	
	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	₹
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	AUTHORS TITLE JOURNAL COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
		Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13305 row: k column: 09 High quality sequence stop: 761.
	FEATURES source	
	BASE COUNT	/olyanism- musculus /db_xref="taxon:10090" /db_xref="taxon:10090" /clone="IMAGE:6051584" /clone_lib="NCI_CGAP_St1" /lab_host="DH10B (T1-resistant)" /lab_host="DH10B (T1-resistant)" /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; /site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.77 kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." 181 a 271 c 258 g 219 t 2 others
	Query » Best Lc Matches	Query Match 31.6%; Score 510.8; DB 14; Length 931; Best Local Similarity 79.9%; Pred. No. 6.5e-69; Matches 634; Conservative 0; Mismatches 138; Indels 21; Gaps 2;
	Qy 272 Db 116	GCAATCCGGTCATACACGGGATCTCTGTGGCAGGAAGGGGGCTGGCT
	Qy 332 Db 171	CGACCTGGCCTGGACTTGCAGGCCATTGAGCTGCCTGCCCAGAGCAACCATCACTGCCAT 391CTGTGGACCTGCCCGCGGTTGAGCTGCCTGCCCAGAGCAACCATTATTGCCAT 223
	Qy 392 Db 224	GCTCAGAAGGGTCCTGACAGTCACTGTGACCCCAAGAAGGGGGAAGGCCCAGCGCCAGCTG 451

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                                      Email: cyapbs-remail.nih.gov
Email: cyapbs-remail.compov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                    mRNA sequence.
BE746716
BE746716.1 GI:10160708
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High quality sequence start: High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3928163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens
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Pred. No. 1.3e-53;
0; Mismatches 72;
                                                                                                      12;
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513 679 479 619 499 420 439 360 379 300

479 559 479 319

259

240

201 120

180

Indels Length

167;

Gaps

7;

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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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BF509598/c
LOCUS
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ORGANISM
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 TATGAAATTGACGGGGGGACCATGCTGATCACGTCGGGCTGCGCTGTGGCTGTGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGAGGAGCACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAG 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCATGGGTGTCCTAGTGGCAGCCTATATT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCAGGAGGAGAACCCAGGGTCGAGCTGCTTCATCCATGTGAATCGGGAATTTAATGCA 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF509598 394 bp mRNA
UI-H-BI4-apf-e-01-0-UI.S1 NCI_CGAP_Sub8
IMAGE:3087073 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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                   65
                                                                                                                                /lab_host="NHIOB (Life Technologies)"
/lab_host="NHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub8
is a subtracted library derived from NCI_CGAP_Sub5. The
NCI_CGAP_Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising: a pool of clones from NCI_CGAP_Sub5 (INAGE
clone Ids 2732833-2737415, 3068040-3069191; 25% of the
driver population), a pool of clones from NCI_CGAP_Sub4
(INAGE clone Ids 2732592-2729326; 25% of the driver
population), NCI_CGAP_Sub6 (pool AIF-AJU, INAGE Ids
2728969-2733190; 25% of the driver population), and
NCI_CGAP_Sub7 (INAGE Ids 3069192-372318, 3081864-3084550;
25% of the driver population). Subtraction was
performed as previously described (Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
                 TAG_LIB=NCI_CGAP_Kid3
TAG_TISSUE=kidney
TAG_SEQ=AATGC"
a 99 c 128 g
                                                                                                    Approaches To Facilitate Gene Discovery. Genome Research 6, \cdot 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3087073"
/clone_lib="NCI_CGAP_Sub8"
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                   102
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Best Local Similarity
Matches 391; Conserv
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AGCTAGTGTGACCCTGAAAAAAAAAAAAAAAAAA 1584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 662)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE741089 662 bp mRNA linear EST 15-SEP-2000 601594088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948165 5',
                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL Plate: LLCM810 row: p column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 648
                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(6). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
                                                                                                                                                                                         /clone="IMAGE:3948165"
/clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 3.
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185 c 241 g 120 t
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Contact: Takao Isc
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Ota,T., Nishikawa,T., Suzuki,Y.,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                     sequence.
AI925963
AI925963.1
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hellx Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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nilarity 99.7%;
Conservative
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/db_xref="taxon:9666"
/clone="PLACE1008371"
/clone_lib="PLACE1"
/tlssue_type="Placenta"
/note="Vector: pME18SFL3"
a 200 c 158 g 114 t
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                                                         319 bp mRNA linear NCI_CGAP_Kidl1 Homo sapiens cDNA clone ITR:Q62941 Q62941 ZINC TRANSPORTER ZNT-2.
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                  BB620842 RIKEN full-length enriched,
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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1 (bases 1 to 319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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81 c 95 g
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/clone_lib="NCI_CGAP_Kidl1"
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/db_xref="taxon:9606"
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Pred. No. 2.9
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mRNA linear ביי ביים.
d, 13 days embryo male testis Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Ko,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sas,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Tel: 81-45-503-9222
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e mouse tissues
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
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               /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissues
                                                                                                                                                                                                                                               /tissue_type="testis"
/dev_stage="13 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus'
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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Sugahara

Aizawa

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Best Local Similarity 76.4
Matches 405; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACGGGGG--GACCATGCTGATCACGTCGGGCTGCGCTGTGGAC 795
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 567)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                musculus cDNA clone C13
BB649221
BB649221.1 GI:16483476
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BB649221 RIKEN full-length enriched, 16
musculus cDNA clone C130062E14 5', mRNA
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Query Match Best Local Matches

Local Similarity

17.2%; 77.7%;

Score 278.4; Pred. No. 2.

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Mismatches

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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y..
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA llbraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                        modified pBluescript KS(+) after
                                                                                                                        was cloned into the XhoI and BamHI sites. Vector:
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/clone="C130062E14"
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Sanger Xenopus tropicalis EST project i
TROPICALIS_SEQUENCE_ID: TGas037a03.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Coconstructed by Maron M. Zorn.
                                                                                                                                                                                                                                                                                                           Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001) Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                          western clawed frog.
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                                                        /dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                   /clone="TGas037a03"
/clone_lib="XGC-gastrula"
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/db_xref="taxon:8364"
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T. Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C. Pertea, G., Holt, I., Karamycheva, S., Llang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                        Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U
                          Email: smith@email.marc.usda.gov
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RESULT 14
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Plate: 58
Seq primer
                                                                                                                                                                 BQ384277
BQ384277.1 GI:21071964
EST.
                                      NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml National Institute of Child Health and Human Development, Naticancer Institute, Xenopus Gene Collection
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                           NISC_mn05g11.y1 NICHD XGC Ov1 Xe IMAGE:5049404 5', mRNA sequence.
              Contact: Robert Strausberg,
                           Unpublished (2002)
                                                                                Xenopodinae; Xenopus.
1 (bases 1 to 608)
                                                                                                                                      Xenopus laevis
                                                                                                                                                   African clawed frog.
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cgapbs-r@mail
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172 c
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Library made from pooled tissue from day 20 and da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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Pred. No. 1.2e-31;
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les 337; Conserv
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                                                                                                                                                                                                GCTGTCATGACTGACGCAGCACCCTGCTCACTGACTTTGCCAGCATGCTCATCAGCCTC
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Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution
Clone distribution: N.A.G.E. Consortium/LLNL at:
                                                                   ENT-2.; mRNA sequence.
BI349390
                                                                                             BI349390 619 bp mRNA linear dac60g08.yl RIKEN Xenopus egg Xenopus laevis cDNA IMAGE:4434615 5' similar to TR:Q62941 Q62941 ZINC
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intram
Xenopus laevis
Eukaryota; Meta
                                                      BI349390.1
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Plate: LLAM11134 ro
                             African clawed frog
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/note="Organ: ovary, Vector: pCMV-SpORT6; Site_1: Not
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 2.0 kb. Constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5049404"
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/sex="female"
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Metazoa;
                                                       GI:15043836
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71.9%;
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Pred. No. 3.5e-30;
0; Mismatches 132
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  Craniata;
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Best Local Similarity 64.3
Matches 397; Conservative
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                                                                                                                                                                                                                                                                      -----AGGAGGAGAACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGAC 910
                                                                            CTTCATCATACAGGGCATGGACACAGTCACGGAACCTGGAAACTCCCATTCTCACTCTCAT 181
                                                                                                                          GATGCTATGCTGATCACCTCTGCCGGGGCAGTTGCAGCCAATATCATAATGGGGGTTAATT 121
                                                                                                                                                                                                                                                                                                                         GGGGTACTGGTGTACCTGGCTGTGGAGCGGCTGATCTCTGGGGGACTATGAAATTGACGGG 754
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
    Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Glibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
    Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality High quality sequence stop: 1.
Location/Qualifiers
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library constructed by Piero Carninci (RIKEN, Genome Science Laboratory, Japan: http://genome.rtc.riken.go.jp/) using egg RNA supplied by Marc Kirschner (Harvard Medical School, Dept. of Cell Biology) DNA Sequencing by: Washington University Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sandy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was amplified at the phage stage and normalized (RoT value = 5). This library was constructed using the CapTrapper method and Trehalose thermoactivated reverse transcriptase to enrich for full-length clones. Library constructed by Piero Carninci (RIKEN, Genome Science Laboratory, Japan: http://genome.rtc.riken.go.jp/) using egg RNA supplied by Marc Kirschner (Harvard Medical School, Dept. of Cell Biology). References: Methods Enzymol.303:19-44 and Genome Res. 10:1617-1630 Please contact Marc Kirschner (marc@hms.harvard.edu) for information on obtaining aliquots of this cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selection was done automatically by the cloning ve
(lambda FIC-II, P. Carninci et al., unpublished).
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/db_xref="taxon:8355"
/clone-"IMAGE:4434615"
/clone_lib="RIKEN Xenopus egg"
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Pred. No. 3.3e-28;
0; Mismatches 197;
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                              CACACCGTGACCATCCAG 1288
                                                                   GCAGACTCGCAAACAGTGCTAAAAAAACGTCAGCTCACAACTACAGAATAAGTTCCACTTT 601
                                                                                                   ACAGACGCCCAGGCTGTGCTGAAGACAGCCAGCCAGCCGCCTCCAAGGGAAGTTCCACTTC 1270
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CACACCACTACTATCCAG 619
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Search completed: March 29, 2003, 22:20:35 Job time: 2987.84 secs

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ATGCAGAGCATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTCAAGCCAGAATACAAG	Score 143.8; DB 4; Pred. No. 5.2e-22; 0; Mismatches 192; GCGTCCGAGCTGCCTTCATCCAT	1461474 1461474 1461474 14709/461,474 1-14 1-14 1-15 1-16	ALIGNMENTS	US-09-665-309-1 US-09-661-569-1 US-09-361-569-1 US-09-365-966-9 US-09-365-966-9 US-09-363-708-3 US-07-920-519-30 US-08-314-586-30 US-08-314-586-30 US-08-314-586-30 US-08-314-586-30 US-09-814-951A-3 US-08-157-101A-4 US-08-974-691-7 US-08-974-691-7 US-08-974-691-7 US-08-308-883-1 US-08-308-883-1 US-08-256-799-1 US-08-256-799-1 US-08-256-799-1 US-08-256-799-1 US-08-256-799-1 US-08-256-799-1 US-08-256-799-1
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Patent No. 6278042
GENERAL INFORMATION:
GENERAL
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SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Plant Metal Transports
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
RUMBER OF SEQ ID NOS: 17
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APPLICANT: Rafalski, Anto
APPLICANT: Sakai, Hajime
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ORGANISM: Oryza sativa
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INFORMATION:
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                                                                                                                                 ATTGAGCGCGAGTAGG
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                                                                                                                                                                                                                                                                                    GGGAAGGTTCTCCTGGCGTGCCATGTGACAATCACTCAGGACGCAGACGCTGATCAAATG
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                                                                                                                                                                      1304
                                     US/09461474
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Pred. No. 1.8e-19;
0; Mismatches 190;
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US-09-461-474-11
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APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 790
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 11, Appl
Patent No. 627804
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                   SEQ ID NO 11
LENGTH: 1208
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Best Local :
                                                                                                                                                                    APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
                                                                                          CURRENT APPLICATION NUMBER: US/09/461, CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
                                                      NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGGGCACTGACGGTGGCCCAGCCTGTTCTGTCTGTCCACATCGCCATTGCTCAGAATA 1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGCTTGAGAGTGGTCTCCGTGAGATGGAAGGTGTGATTGCGGTCCATGAGCTGCACA
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                                                                                                                                                                                                                                                                                                    Application US/09461474
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Pred. No. 1.3e-16;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (471)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown US-09-134-001C-30
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; Sequence 30, Application US/09134001C
; Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 237; Conserv
                                                                      Matches
                                                                                                                                                                                                                                                                                   SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GTC-007
                                                                                                                                                                                                                           LENGTH: 504
TYPE: DNA
ORGANISM: Staphylococcus
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                      CCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAGAGCATGGGTGT 930
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CCTCAGCACGCGCCTGCCCTCGTGCATGTGATGGGAGACTTGCTCGGCTCGGTCGCCGG 65
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                                                                      176; Conser
                                                                      Conservative
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                                                                    Score 68.8; DB 4;
Pred. No. 3.9e-06;
0; Mismatches 157
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Pred. No. 5.2e-14;
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                                                                      157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application PC/TUS9506406A GENERAL INFORMATION:
APPLICANT: Janet D. Robishaw, Charl
                                                  Matches
                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
1501 TCCCAGCCTCCCATCTGACTACAGCCAGGGTGGGGGACTCAGCGGGTATAAAAGCTAGTGTG 1560
                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE
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                                                                                                                                                                        TYPE: Nuclei
STRANDEDNESS:
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                                                Local Similarity 71.7 cs 81; Conservative
                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                Score 61.8; DB 5;
Pred. No. 0.00014;
0; Mismatches 32;
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US-08-802-805D-20
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                                                                                                          GENERAL INFORMATION:
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                                                                                                                       Sequence 1, Application US/09394645 Patent No. 6380371
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                           APPLICANT: Sassetti, Christopher M.
APPLICANT: Rosen, Steven R.
TITLE OF INVENTION: Endoglycan: A NOVEL PROTEIN HAVING SELECTIN
TITLE OF INVENTION: LICAND AND CHEMOKINE PRESENTATION ACTIVITY
FILE REFERENCE: 6510-122US1
 CURRENT APPLICATION NUMBER: US/09/394,645 CURRENT FILING DATE: 1999-09-13
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: TOTChia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
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Local Similarity 62.8%;
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5 San Francisco
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.0009;
Pred. No. 54;
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Best Local Similarity
Matches 93; Conserv
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Best Local Similarity
Matches 93; Conserv
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                                                                                          Sequence 1, Application US/08706216 Patent No. 6140098
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CURRENT FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: US 60/074,389
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APPLICANT: Sassetti, Christopher M.
TITLE OF INVENTION: No. 6395882el Selectin Ligands
FILE REFERENCE: UCAL097US1
                                                            GENERAL INFORMATION:
APPLICANT: Balasu
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: human
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
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   I: Zurawski,
INVENTION:
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                              Gorman, Daniel M.
                                               Ford, John
                                                            Balasubramanian, Sriram
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Pred. No. 0.
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Pred. No. 0.002;
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   RELATED REAGENTS
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NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS

ADDRESSEE:

Palo Alto

901 California Avenue

DNAX Research Institute

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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/09020956 Patent No. 6261562
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2719 base pairs
      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION: TELEPHONE: 415-852-9196
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                     2698 AAAAAA 2703
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LOCATION:
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ZIP: 98104
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                                                                                                                                                                Seattle
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                                                                                                                                                                                 701 Fifth Avenue
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-030-607-32
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Best Local Similarity
Watches 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-09-020-956-32
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 789 base pairs
                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1503 CCAGCCTCCCATCTGACTACAGCCAGGGTGGGGACTCAGCGGGTATAAAGCTAGTGTGAC 1562
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                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                       FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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EDNESS: single
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Pred. No. 0.0026;
0; Mismatches 3
 Score 55.8; DB 4; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701 Fifth Avenue
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              Length 789;
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US-09-605-785-32/c
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US-09-605-785-32
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                                                                                        Sequence 32, Application US/09439313 Patent No. 6329505
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      Matches
APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan Lou APPLICANT: Jiang Yuqui
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CURRENT FILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 789
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                     1503 CCAGCCTCCCATCTGACTACAGCCAGGGTGGGGACTCAGCGGGTATAAAGCTAGTGTGAC 1562
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Kalos, Michael
                  Harlocker, Susan Louise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick,
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Pred. No. 0.0026;
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US-09-352-616A-32/c
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                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/352,616A CURRENT FILING DATE: 1999-07-13 NUMBER OF SEQ ID NOS: 472 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 32 LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
                                                                 Best Local Similarity Matches 75; Conserv
                                                                                                Query Match
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS F
FILE REFERENCE: 210121.427C8
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CURRENT APPLICATION NUMBER: US/09/439,313
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ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C
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                               1503 CCAGCCTCCCATCTGACTACAGCCAGGGTGGGGACTCAGCGGGTATAAAGCTAGTGTGAC 1562
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129 CCTGTTGCCGTCCTGTCCCCAGCCTGNTTGTGTCCCGNGAGGTTGTCAATAAACCTGCCC 70
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1 Similarity 67.6%;
75; Conservation
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                                                                 Conservative
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                                                                 Score 55.8; DB 4;
Pred. No. 0.0026;
0; Mismatches 36;
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Maximum Match 10
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Sequence 41, Appl
Sequence 20, Appl
Sequence 13, Appl
Sequence 522, App
Sequence 21, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 54, Appl
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Sequence 126, Appl
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Sequence 17, Appl
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sequence 31, Appi	31,	-	31,	31,	Sequence 31, Appl	31,	31,	31,	31,	-	•	е 3,	11,	11, 1	231, Ap	Sequence 6165, Ap	•	32,	•	32,	e 32,	32,	,	Sequence 32, Appl	Sequence 32, Appl

ALIGNMENTS

RESULT 1 US-10-162-012-39

Sequence 39, Appropriate Publication No.

Application US/10162012 No. US20030051660A1

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GENERAL IMPORMATION:

APPLICANT: Cutils, Roty A.J.

APPLICANT: Gutils, Roty A.J.

APPLICANT: GLOR-Santlago, Inmaculada
APPLICANT: GLOR-SANTLAGO, INMACULAGO
FILE REFERENCE: 10448-190001

CURRENT APPLICATION NOMBER: US(10/162,012

CURRENT FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US(10/162,012

PRIOR APPLICATION NUMBER: US(10/1834)

PRIOR APPLICATION UMBER: US(10/1834)

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ORGANISM: Homo
FEATURE:
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OR FILING DATE: 2001-03-28
OR APPLICATION NUMBER: US 10/109,029
OR FILING DATE: 2002-03-28
OR APPLICATION NUMBER: PCT/US02/09728
OR FILING DATE: 2002-03-28
OR APPLICATION NUMBER: US 60/290,288
OR FILING DATE: 2001-05-11
OR APPLICATION NUMBER: US (not assigned)
OR FILING DATE: 2002-05-13
BER OF SEQ ID NOS: 48
TWARE: FastSEQ for Windows Version 4.0
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        ATCTGGGTCGTGACGGGGGTACTGGTGTACCTGGCTGTGGAGCGGCTGATCTCTGGGGAC
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Sequence 41, Application US/10162012
Publication No. US20030051660A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: GU, Wei
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AN
FILE REFERENCE: 10448-190001
CURRENT APPLICATION UNMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-04 RESULT 2 US-10-162-012-41

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Best Local Similarity
Matches 1118; Conserv
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OR APPLICATION NUMBER: US 60/209,238
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OR APPLICATION NUMBER: US 09/875,363
OR FILING DATE: 2001-06-05
OR APPLICATION NUMBER: PCT/VS01/18247
OR APPLICATION NUMBER: PCT/VS01/18247
OR FILING DATE: 2001-06-05
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RE FILING DATE: 2000-06-05
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                                                                                                                                                                                                                                                                                      Score 1117.4; DB 9
Pred. No. 1.1e-280;
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                                     CTCCAAGGGAAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGAC
                                                 CTCCAAGGGAAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGAC
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US-09-872-153-20

Sequence 20, Application US/09872153

Patent No. US20020082207A1

GENERAL INFORMATION:

APPLICANT: Hists, Shannon K.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.531

CURRENT APPLICATION NUMBER: US/09/872,153

CURRENT FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 28

SOSTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 2852
; TYPE: DNA
; ORGANISM: Homo s
US-09-872-153-20
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AGCTTTACGATGCACTCACTCACATTCAGATGGAATCTCCAGTTGACCAGGACCCCGAC
                         AAGTTCCACTTCCACACCGTGACCATCCAGATCGAGGACTACTCGGAGGACATGAAGGAC
                                                                          GGCGTTGACTCTCACAGCTGTTCGTGATCTGCTGCTGTCGGAGGGGGTAGAAGCCCCTG
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                                                   ACAGCAGCCAGCCGGGACAGCCAAGTGGTTCGGAGAGAATTGCTAAAGCCCTTAGCAAA
                                                                                                       CACAGCCTGCACATCTGGTCTCTAACAATGAATCAAGTAATTCTCTCAGCTCATGTTGCT
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Pred. No. 1.3e-70;
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; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo s
US-09-957-708-13
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TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Genes
FILE REFERENCE: DEX-0339
CURRENT APPLICATION NUMBER: US/09/957,708
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,746
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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Best Local
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APPLICANT: Reci
APPLICANT: Caff
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                                                                              GAGGAGAACCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTTATGCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCTTTTCTGTGAAGACCCCTGTGACTAGCT
 GTTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAATACAAGATTGCTGAC
                  ATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTCAAGCCAGAATACAAGTATGTAGAC
                                                          CAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGAGATCTGGTACAGAGT
                                                                                                                    TCCCACTCCCTGCCTTCAAATTCCCCCTACCAGAGGTTCTGGGTGTGAACGTAACCATGGG
                                                                                                                                                     GGCACCACC----
                                                                                                                                                                                GTGGCTGTGAACATCATAATGGGGTTGACCCTTCACCAGTCTGGCCATGGGCACAGCCAC
                                                                                                                                                                                                                                            ACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATCACCGCAGCTGTTGGA 944
                                                                                                                                                                                                                                                            CTGATCTCTGGGGACTATGAAATTGACGGGGGGACCATGCTGATCACGTCGGGCTGCGCT
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Cafferkey, Robert
Ali, Shujath
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Pred. No. 7.2e-36;
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700342872H1
LOCATION: 235
OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-294-093B-522
; Sequence 522, Application US/09294093B
; Patent No. US20010051335A1
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LENGTH: 278
TYPE: DNA
              Sequence 21, Application US/09982809
Patent No. US200201066/BAI
GEMERAL INFORMATION:
APPLICANT: ROBISHAW, JANET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR EILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ito, Laura, Y.

APPLICANT: Sherman, Bradley, K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                            974 TATGTAGACCCCATCTGCACCTTCGTCTTCTCCATCCTGGGGACAACCTTGACC 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                     854 AACCAGCAGGAGAACCCCCAGCGTCCGAGCTGCCTTCATCCATGTGATCGGCGACTTT 913
                                                                                                                                                                                                                                                                                                                                                                         914 ATGCAGAGCATGGGTGTCCTAGTGGCAGCCTATATTTTATACTTCAAGCCAGAATACAAG 973
                                                                                                                                                                                                                                                       165 GTCATCGACCTCATCTGCACGCTCGTCTTCTCGGTGGTGGTGCTGTTCACCACGATCCGG
                                                                                                                                                                                                                                                                                                                                                                                                              45 AAGAAGCCTCGGCGGAACATCAACGTGCACAGCGCATACCTCCACGTGCTCGGGGACTCC 104
                                                                                                                                                                           ATGCTGCG-CANATCCTCGAAGTGTTGATGGAGAGCACGCCCCGCGAGATCGAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCATCTGCACCTTCGTCTTCTCCATCCTGGTCCTGGGGACAACCTTGACCATCCTGAGA 1042
                                                                                                                                                                                                              ATCCTGAGAGATGTGATCCTGGTGTTGATGGAAGGGACCCCCAAGGGCGTTGAC 1087
                                                                                                                                                                                                                                                                                                                                    GTCCAGAGCGTCGGGGTCATGGTGGGGGGGGGGGGATCATCTGGTACAAGCCGGAGTGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTCAGGAAAATCTACTGCCATAGTTCACAT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTAAATATCTGGTCTCTC 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCTGCTGCTGTCGGTGGAGGGGGTAGAAGCCCTGCACAGCCTGCATATCTGGGCACTG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAATGTAGACTATATCAAA 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACATTTCGAATCATATGG
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KUNSCH,
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CHARLES
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Pred. No. 9.4e-10;
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                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                       SEQ ID NO 19
LENGTH: 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local
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SEQ ID NO 21
                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/134,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/982,809
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 08/952,772
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: PCT/US95/06406
PRIOR FILING DATE: 1995-05-22
                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CDNA CLONES ENCODING HUMAN GFILE REFERENCE: P50339
                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                           NAME/KEY: SITE
LOCATION: (1253)
OTHER INFORMATION: n
                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (1252)
OTHER INFORMATION: n equals a,t,g,
                                                                                                              OTHER INFORMATION: n
                                                                                                                            NAME/KEY: SITE LOCATION: (1254)
                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
1465 CTCCTGACCTCTGCCCCACTCCAGGAATGGAGCTCTTCCCAGCCTCCCATCTGACTACAG 1524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1501 TCCCAGCCTCCCATCTGACTACAGCCAGGGTGGGGACTCAGCGGGTATAAAGCTAGTGTG 1560
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                               Local Similarity
les 94; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCAGTCTCACCTGGAGCTACTGGGAGGGTAAAGCCCATTTGAAGAATAAAGTCATCCAG
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                                                                                                                                                                                                                                                                                                                                      PatentIn Ver.
                                 Conservative
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                                             3.8%;
                                                                                                           equals a,t,g,
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                                              Score 61;
Pred. No.
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                               Mismatches
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                               . 3.7e-06;
cches 55;
                                                              DB 9;
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                                                              Length 1254;
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                                 Indels
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CTCCAGATCTCAACCTGTTCCCTGGAAGTAGGGCCTGCTCCCATCCCAGTGAAATAAAC

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US-10-033-350-1
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                                                                                                                                                                                     Query Match
Best Local Similarity bacc
91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                   2216
                                                                                                     1529
 2276
                                                                                                                                      1469 TGACCTCTGCCCCACTCCAGGAATGGAGCTCTTCCCAGCCTCCCATCTGACTACAGCCAG 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/860,370
FILING DATE: - CIDKNOWND
APPLICATION NUMBER: PCT/US97/04363
FILING DATE: 13-Mar-1997
APPLICATION NUMBER: 08/615902
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: 08/618236
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: TOICHIA, PhD., Timothy E. REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 90996P1PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR NUMBER OF SEQUENCES: 12
AAAAAAAAAAAAAAAAAAAAA 1613
                                                                                                 АААААААААААААААААААААА 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/033,350 FILING DATE: 02-No. US20030022284A1-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Double TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ryan, Anne M.
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                                                                                                                                                                                                                      3.6%;
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                                                                                                                                                                                                      Score 58.6; DB 9;
Pred. No. 2e-05;
0; Mismatches 54;
                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                        Length 2378;
                                                                                                                                                                                                        Indels
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 54
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-846-54
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US-10-091-483-126
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US-10-091-483-54
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Best Local S
Matches 63
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NUMBER OF SEQ ID NOS: 348

Prior Application removed - See File Wrapper or Palm SOETWARE: PatentIn Ver. 2.0

SEQ ID NO 54

LENGTH: 307
Sequence 126, Application US/10091483
Publication No. US20030049650A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54, Application US/09764846 Patent No. US20020102638A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54, Application US/10091483 Publication No. US20030049650A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Matches
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CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - NUMBER OF SEQ ID NOS: 348 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/764,846 CURRENT FILING DATE: 2001-01-17
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 1.1e-05;
0; Mismatches 8;
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Pred. No. 1.1e-05;
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OTHER INFORMATION: n equals a,t,9, o.
NAME/KEY: misc_feature
LOCATION: (309)
OTHER INFORMATION: n equals a,t,9, o.
NAME/KEY: misc_feature
LOCATION: (314)
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
Prior Application removed - See File Wrapper or Palm SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 126
LENGTH: 314
                                                                                                   Query Match
Best Local
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SEQ ID NO 126
LENGTH: 314
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Best Local S
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CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (314)
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LOCATION: (309)
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OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: SITE
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                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, or
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Pred. No. 1.1e-05;
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; Publication No. US20
; GENERAL INFORMATION
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ELENGTH: 371
TYPE: DNA
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 371
TYPE: DNA
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CURRENT FILING DATE: 2001-08-10
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NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-08-10
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LOCATION: (350)
OTHER INFORMATION: n equals a,t,g,
                  OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature LOCATION: (360)
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OTHER INFORMATION: n equals a,t,g,
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Pred. No. 1.
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US-09-925-299-16

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TYPE: nucleic acid
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STRANDENNESS: double
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TOPOLOGY: linear
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MOLECULE TYPE: CDNA
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SEQUENCE DESCRIPTION: SEQ ID NO: 149:
US-09-745-763-149
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                                                                                                       Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                 NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
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Best Local Similarity 91.0%;
Matches 61; Conservative
1585 АВААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 1613
                                    1607 AAAAAAA 1613
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Oun-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
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                                                                                                           Conservative
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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                                                                                                       3.5%; Score 57; DB 10; Length 1152; 77.5%; Pred. No. 3.9e-05; tive 0; Mismatches .20; Indels
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Pred. No. 1.9e-05;
0; Mismatches 6;
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Db 1088 AAAAAAAAAAAAAAAAAAAAAAAAAAA 1116

Search completed: March 30, 2003, 01:54:56 Job time: 191.281 secs

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Minimum |
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 000 0.0 0000 C 000 No. 230 227.6 226.6 226.6 226.4 226.4 225.6 225.6 225.6 225.6 225.6 225.6 225.6 225.6 225.6 225.4 22 Score 000 Query Match 340000 25233 145050 144555 154918 189536 191722 168006 157463 286758 187984 16781 150336 88665 152121 152121 152121 152121 152121 194310 146017 39673 8737 100000 100000 14 3 3 3 5 11 0 9 6 5 17 8 4 5 1 16 7 9 2 4 12 9 0 4 3 3 7 7 8 4 9 8 7 1 3 17 2 2 0 3 4 4 1 8 3 194191 32289 186625 170862 110233 142728 209856 Length DΒ AC124853 HSDJ792G4 AC010330 AC091529 AC006449 AP001262 AL356422 HSJ395C13 AP001261 AP001261 AL139396 AC067891 CNS01DTD AX411375 AL391650 AC097332 AC093822 AC006487 AC015795 AC025188 AC025188 AC021078 AC037451 AL1138781 AC117834 AC116360 AC126227 AC007686 AC018500 AC097359 AC090543 AC073177 AP001716 AL591212 AP000110 AP000186 AL672238 AP000289 AP000042 AC005863 AC093229 AC002997 AC002511 Ħ AC093822 Homo sapi AC015795 Homo sapi AC015795 Homo sapi AC025188 Homo sapi AC025188 Homo sapi AL139396 Human DNA AC067891 Homo sapi AL1393712 Human DNA AC00297 Human DNA AC00297 Human DNA AC002511 Human DNA AC002513 Homo sapi AC124853 Homo sapi AC193229 Homo sapi AC193229 Homo sapi AC091529 Homo sapi AC091529 Homo sapi AC091529 Homo sapi AC091529 Homo sapi AC006449 Homo sapi AC016261 Homo sapi AL117344 Human DNA AL117344 Human DNA AL117344 Homo sapi AP0001267 Homo sapi AP001267 Homo sapi AC027473 Homo sapi AC027473 Homo sapi AP000116 Homo sapi AC021078 AC037451 AL138781 AC117834 AC116360 AC126227 AC007686 Description Homo sapi Human DNA Homo sapi Homo sapi Papio cyn Homo sapi Homo sapi Homo sapi Sequence Human DNA Pan trogl

ALIGNMENTS

RESULT 1
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LOCUS
Sequence 3 from Patent w00224910.
AX411375
VERSION
AX411375
VERSION
AX411375
Numan.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE
AUTHORS
AUTHORS
TITLE

Wei, M.H., Ketchum, K.A., di Francesco, V. and Beasley, E.M.
Isolayed human transporter proteins, nucleic acid molecules
encoding them, and uses thereof

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                  AAACCAGAGTCCAGAGAAGCAGAGGGCACTCAGTGAGGACCCAAGCAGAGCGGGTGCAC
                                                 GCTGGTGCTCAGAGTAGACAGACCTGGAGAAAACCAGGGTGTCTGAGGTTTTTCCAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCACATCCTCACTCCTGGCACCCCGTCTCCTACAAGATGAGAGACCGAAAGAGCCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 15, 2001 this sequence version replaced gi:16605685. During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-96L14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP11-96L14 The true left end of clone RP11-231P20 is at 72881 in this sequence. The true right end of clone RP11-111D20 is at 72886 in this sequence Location/Qualifiers
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/note="Sequence from uni-directional
terminator reads only."
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/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-96L14"
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  Score 1000; DB 9;
pred. No. 2.5e-269;
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Bryant, N.P., Banks,T.,

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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Carlo, M., Christopoulos, C.,
Chen, G., Chen, R., Carlo, M., Dathorno, S. Bould, M., Chen, C., Chen, R., Charlo, M., Dathorno, S. Bould, M., Charlo, C., Chen, C., Chen, C., Chen, C., Chen, C., Charlo, M., Dathorno, S. Bould, M., Charlo, C., Chen, C., Ch
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On Jun 13, 2002 this sequence version
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Center project Information Center project name: ZUAZ Center clone name: RP43-22B16
                                                                          Web site: http://www.hgsc.bcm.
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                             Center: Baylor College of Medicine
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                                                                                        GAGTTCAAGACCAGCCTGGCCAACATGGTGAAAAGCCTATCTCTACTAAAAACTACAAAAAAT 13231
                                                                                                                ACCCAGATGACATTTATCCCTAAATACTTTAGATAAAGGTGTTCTTTGAAAAAAATCAT 356
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Similarity
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 193448 bases at least Q40
Consensus quality: 193860 bases at least Q30
Consensus quality: 194094 bases at least Q20
Estimated insert size: 194270; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8.5x in Q20 bases; sum-of-contigs estimation
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/db_xref="taxon:9598"
/clone="RP43-22B16"
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75717: gap of unknown length
132426: contig of 56709 bp in length
132526: gap of unknown length
130942: contig of 48416 bp in length
181042: gap of unknown length
183092: contig of 2050 bp in length
183192: gap of unknown length
184191: contig of 10999 bp in length
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Pred. No. 2e
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132311

132252

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions

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                                                                                                        Direct Submission
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Feb 5, 2002 this sequence version replaced gi:15529861.
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Homo sapiens BAC clone RP11-382L24
AC093822 AC036160
AC093822.2 GI:18497235
                                                                                                                                                                                                                            Direct Submission
Direct Submission
Submitted (08-FEB-2002) Department of Genetics,
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Submitted (05-FEB-2002) Genome
University School of Medicine,
MO 63108, USA
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Center project name: H_NH0382L24 Drafting Center: WIBR
                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
restriction digest.
                                                                                                                                                                                 quality >=
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MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-32C8, 2000 bp overlap; the clone sequenced to the right is RP11-541E12, 2000 bp overlap. Actual end of this clone is at base position 37821 of RP11-541E12.

Single stranded/single chemistry coverage below phred30, base position 19583 to 19596.

A trasposon was identified in the vector sequence of the clone ${\tt RP11-382L24}$.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-382L24"
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/db_xref="taxon:9606"
/chromosome="2"
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              _family="(T)n'
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Best Local Similarity

23.5%;

Score 234.6; DB 9 Pred. No. 9.4e-55;

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Length 32289;

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17089. .17130
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5058. .5255
17445. .17581
/rpt_family="L1"
17448. .17470
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Unpublished
2 (bases 1 to 186625)
2 (bases 1 to 186625)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Cooke, P., Deval, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Galdyna, S., Gilbert, D., Grant, G., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Maronis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anders, Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, J. Bastle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Costle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, M., Forrest, C., Eunko B., Garen, T., Calagan, T., Cardyna, S., Gilbert D., Grant, C., College, M., Ferreira, P., Fitzhugh, M., Forrest, C., Eunko B., Garen, T., Cardyna, S., Gilbert D., Grant, C., College, M., Ferreira, P., Fitzhugh, M., Forrest, C., Eunko B., Garen, T., Cardyna, S., Gilbert D., Grant, M., College, M., Ferreira, P., Fitzhugh, M., Forrest, C., Eunko B., Garen, T., Cardyna, S., Gilbert D., Grant, M., College, M., Forreira, P., Fitzhugh, M., Forreira, C., Fitzhugh, M., Forrest, C., Funda, M., Forreira, P., Fitzhugh, M., Forreira, P., Funda, M., Forreira, P., Fitzhugh, M., Forreira, P., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-NOV-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 9, 2000 this sequence version replaced gi:4314418. All repeats were identified using RepeatMasker: Smit, A.F.A. &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-MAR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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3609. 3886
                                                                                                                                                                               /rpt_family="Alur"
complement(3306..3492)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(295
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2012. 2102
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                                                 /rpt_family="(CAAA)n"
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8706
                                                              /rpt_family="(TCCTG)n"
complement(25798. .25885)
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complement(17230. .17)
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5. .13904)
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18387
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Matches 378
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nes 378; Conserv
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Conservative
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31657. .31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(36458. .36714)
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/rpt_family="L2"
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complement(31245. .31424)
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31487. .31656
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complement/35000
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complement/or-
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complement(20700
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31968. .32115
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Pred. No. 2.2e-53;
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Rirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meddrim, J., Morman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Koy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Titrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Varman n., Vau, T., Immer A., and Zodv. M.
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                                                                                         Boukhgalter, B., Brown, A., Cammarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Faros, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Faros, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Faros, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Faros, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Faros, B., Faros, B., Faros, B., Faros, B., Faros, B., Faros, B., Faros, Faros,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 170862)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
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Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 170862)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
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> McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
> Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
> Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
> Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
> Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
> Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
> Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
> Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
> Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
> Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

Submitted (24-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 24, 2002 this sequence version replaced gi:19683229. http://ftp.genome.washington.edu/RM/RepeatMasker.html ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research repeats were identified using RepeatMasker: t, A.F.A. & Green, P. (1996-1997) Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu Center code: WIBR

REFERENCE AUTHORS

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION COCUS AC015795 RESULT 6

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complement(2341... complement(5489. /rpt_family="Alusg"
complement//> /note="<30 qual SNGL region" 3422. .3736 2381. .2385 /note="<30 qual SNGL region" 2448. .2452 complement(785 Location/Qualifiers rpt_family="L2" /rpt_family="AluY" /rpt_family="(TA)n" /map="17" /db_xref="taxon:9606" rpt_family="HAL1b" rpt_family="Alusc" /rpt_family="LlME4A" rpt_family="Alusx" rpt_family="(TTTC)n" rpt_family="L2" rpt_family-"FLAM_A" clone_lib="RPCI-11 Human Male BAC" /clone="RP11-613C6" 'chromosome="17" organism="Homo sapiens" .170862 _family="AluSp" _family-"L1ME4A" _family="L2" .4909 .1044 2054 .5662) .2633)

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                                                                                                                      Score 228; DB 9; : Pred. No. 7.9e-53; 0; Mismatches 210;
                                                                                                                                           Length 170862;
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (bases 1 to 143335) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                             Submitted (12-DEC-2001) DOE Joint Genome Institute, 2800 M Drive, Walnut Creek, CA 94598, USA On Dec 12, 2001 this sequence version replaced gi:16328263 Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                  Submitted (23-OCT-2001) DOE Joint Genome Institute, 2800 Mil Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 14335)
DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143335 bp DNA linear PRI 12-DEC-
Homo sapiens chromosome 5 clone CTD-2384B11, complete sequence.
AC025188
                                                     Quality: Phrap Quality >=40 99.9% of Sequence.
Estimated Total Number of Errors is 0.1.
Location/Qualifiers
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DOE Joint Genome Institute.
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                                                                                                                   www-shgc.stanford.edu
                                                                                                                                         Finishing Completed at Stanford Human Genome Center
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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             BOE
                                                                     Mammalia; Eutheria; Primates;
1 (bases 1 to 110965)
DOE Joint Genome Institute.
                                                                                                                                                                                                                ACU2U927 110965 bp DNA linear Homo sapiens chromosome 5 clone CTD-2153E7, WORKING
                                                      Sequencing of Human Chromosome
                                                                                                               Eukaryota; Metazoa; Chordata;
                                                                                                                               Homo sapiens
                                                                                                                                                       AC020927.4 GI:7711631
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
                                          Jnpublished
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            (bases 1 to 110965)

Joint Genome Institute
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/clone="CTD-2384B11"
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Pred. No. 1e-52
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                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae
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Best Local Similarity
Matches 373; Conserv
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                                                                                                                                         TTTATTTCTTCTATACCAGTACCGTACTCTCCCCACTGGGATTATTTTAAGGCAAAACCC
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                                             AGATGACATTTTATCCCTAAATACTTTAGATAAAGG--TGTTCTTTGAAAAAAATCATAA 358
                                                                                            TGAATCTTTGCCCCAAGAAATCTGTGTTTTTAACAAGTTTCTCAGGCCAGGTGCGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* 8728: contig of 8728 bp in length

* 8729 8828: gap of unknown length

* 8829 11329: contig of 2501 bp in length

* 11330 11429: gap of unknown length

* 11430 40589: contig of 70276 bp in length

* 40590 40689: gap of unknown length

* 40590 119955: contig of 70276 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 106980 bases at least Q40 Consensus quality: 109994 bases at least Q30 Consensus quality: 110455 bases at least Q20 Estimated insert size: 110000; pulse field gel estimation Estimated insert size: 110815; sum-of-contigs estimation Quality coverage: 7.03 in Q20 bases; pulse field gel estimation Quality coverage: 6.98 in Q20 bases; pulse field gel estimation.
* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs estimation.
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center Project Name: 686404
Center clone name: CITB-H1_2153E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Project Information
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/chromosome="5"
/clone="CTD-2153E7"
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23208 c 24149 g 31014 t 300 other
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Pred. No. 1.9e-52;
0; Mismatches 199
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                                                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 1, 2002 this sequence version replaced gi:10862725.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
                                                                                                                                                                                                                                     one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-258C19 is from the library RPCI-11.1 constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone RP11-258C19 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 178451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL139396 178451 bp DNA Human DNA sequence from clone RP11-258C19 XP11.21-11.23, complete sequence.
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                                                                                                                                                                                                                      further details see
                                                                                                                                                                                                  //www.chori.org/bacpac/home.htm
                                                                                                                                                                               pBACe3.6.
/clone="RP11-258C19"
/clone_lib="RPCI-11.1"
178349. .178451
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                         /map="p11.21-11.23"
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (28-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, shire, CB10 1SA, UK. E-mail enquiries:
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Query Match
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                                                             Mammalia; Eutheria; Primates; Catarrhini; Hom:
1 (bases 1 to 167924)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-342J16
unpublished
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AC067891.5 GI:14670136
AC067891.5 GI:HTGS_DRAFT; HTGS_FULLTOP
2 (bases 1 to 167924)
Birren,B., Linton,L.,
Anderson,S., Baldwin,J
                                                                                                                                                                                                                                                                                                                      SEQUENCE,
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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  Baldwin,J.,
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    Nusbaum,C., Lander,E., Abraham,H.,
J., Barna,N., Bastien,V., Beda,F.,
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17, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; M77815; 2% of reads
Sequencing vector: M13; M77815; 2% of reads
Sequencing vector: Plasmid; n/a; 98% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 166252 bases at least 040
Consensus quality: 166252 bases at least 030
Consensus quality: 166252 bases at least 020
Insert size: 170000; agarose-fp
Insert size: 170000; agarose-fp
Insert size: 1170000; agarose-fp
Quality coverage: 11.6 in 020 bases; agarose-fp
Quality coverage: 11.6 in 020 bases; agarose-fp
Quality coverage: 11.6 in 020
**NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
** 1977. Contict of 027 be 100% of 1
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All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 342_J_16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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38 937: gap of 100 bp
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7424 7523: gap of 100 bp
7524 15931: contig of 8408 bp in length
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                                                         /clone="RP11-342J16"
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/chromosome="17"
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clone_lib="RPCI-11 Human Male
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                                                                              CNS01DTD 129043 bp DNA linear PRI 02-MAY-2001
Human chromosome 14 DNA sequence BAC C-2134A5 of library CalTech-D
                  HIG
                                AL132712.4
                                                               from chromosome 14 of Homo sapiens (Human), complete sequence
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1 (bases i to 129043)

Heilig.R., Petit.J.L., Vico.V., Dasilva.C., Robert.C., Wincker.P., Brottler.P., Cattolico.L., Barbe.V., Pelletier.E., Artiguenave.F., Levy.M., Eckenberg.R., Bruls.T., deBerardinis.V., Cruaud.C., Gyapay.G., Saurin.W. and Weissenbach.J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overall quality chart : Range : bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following BAC sequence is oriented from the T7 to the Upstream BAC (overlapping the T7 end): R-865F7 (AC-AL1360 Downstream BAC (overlapping the SP6 end): R-73M18 ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web: www.genoscope.cns.fr)On May 7, 2001 this sequence version replaced gi:11611133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-MAY-2001) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage:
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RHdb:RH75092
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RHdb:RH53663
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                                                                                               RHdb:RH32321
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/db_xref="taxon:9606"
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Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K., Garcia, E., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A. Olsen, A.O. and Carrano, A.V.
Submitted (07-OCT-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from centromere to telomere.
                                                                                                                                                                                                                                                                                                              Human DNA from chromosome 19-specific cosmid R26667, sequence, complete sequence. AC002997
                                                 Lamerdin, J.E.
Direct Submission
                                                                                                Sequence analysis of a 
Unpublished
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/note="predicted exon, program: grail2exons_human_1.3,
/rame: 1, quality: marginal, score: 49.000"
complement(4383. .4678)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                            frame: 2, quality: excellent, score: 85.000* 10463. .10759
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2897. 3360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
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/clone_lib="LL19NC03 R chromosome 19-specific cosmid
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/clone="R26667"
                                                                                                                                            frame: 2, quality: 16106. .16395
                                                                                                                                                                                                                                                       frame: 2, quality:
12808. .13086
                                                                                                                                                                                                                                                                                  /note="predicted exon,
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good, score:
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excellent, score: 92.000"
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64.000"
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/mote="predicted exon, program: gi
/note="predicted exon, program: gi
frame: 0, quality: good, score: 6:
complement(28907, .29188)
/rpt_family="Alu"
29333, .29428
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complement(29828. .30
/rpt_family="Alu"
30963. .30998
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/note="DDS similarity to T03155 FB26A8 Fetal brain,
Stratagene Homo sapiens cDNA clone FB26A8 3'end (1.
score: 581 Identity: 313/327 (95%)"
25560. .25849
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36565.
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frame: 0, quality: excellent, score: 85.000"
complement(35688. .35869)
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complement(34242.
/rpt_family="Alu"
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/note="predicted exon, program:
frame: 1, quality: good, score:
complement(28345. .28635)
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/rpt_family="Alu"
20491. .20791
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34671. .34879
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                                                                                                                                                                                            Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K., Garcia, E., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, Olsen, A.O. and Carrano, A.V. Sequence analysis of a 1Mb region in 19q13.1
                                                                                       Submitted (28-AUG-1997) Human Genome National Laboratory, 7000 East Ave., Location/Qualifiers
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98713)
                                                                                                                                                                                                                                                                                                                                                                                Human DNA from chromosome 19-specific PAC PC28130, sequence, complete sequence.

AC002511
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Homo sapiens
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                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="overlaps cosmid F16632
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                                                                                                                                                                                                              /note="BLASTX similarity to P34976 (50. 215); match: 0.26, score: 5.8e-13; database searched: nr: TYPE-1 ANGIOTENSIN II RECEPTOR (AT1) pir[|A48857 AT1 angiotensin II receptor - rabbit >gi|299615 (559041) AT1" complement(5988. 6380) /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 77.000"
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3453. .3740
                                                                                                          /replace="G in cosmid 6247...6333
                                                                                                                                                                                                                                                                                                                                                                                                17160-20068 on 3'-side"

complement(5499. .5778)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 85.000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3990. .4054)
/note="predicted exon, program:
frame: 2, quality: good, score:
complement(4210. .4312)
/note="predicted exon, program:
frame: 2, quality: excellent, so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ch19 cosmid f16632"
/replace="A in cosmid (base
complement(2925...3242)
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2741
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/rpt_family="Tigger2"
1479..1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
1057. .1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /replace="C in cosmid (base 30668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Tigger2"
complement(261. .730)
/rpt_family="Tigger2"
complement(760. .1013
                  /note="BLASTX similarity to P34976 (290..318); match:
0.31, Score: 5.8e-13; database searched: nr; TYPE-1
ANGIOTENSIN II RECEPTOR (AT1) pir[|A48857 AT1 angiotensin
II receptor - rabbit >gi|299615 (S59041) AT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(69.
                                                                                                                                                    /standard_name="polymorphism"
/clone="ch19 cosmid f16632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="polymorphism in length of Alu tail"
/clone="ch19 cosmid f16632"
/replace="two fewer A's in cosmid at base 29187-29188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="fibroblast"
/cell_type="fibroblast"
/note="see Ioannou et al.(1994) Nature Genetics 6: 84-89
for more information regarding PAC library construction."
8. .67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="oriented from
/clone="PC28130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4688-7614 on 5'-side of insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="duplication flanking
10 kb DNA insertion in PAC clone relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name="duplication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
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/clone="ch19 cosmid f16632"
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                                                                                                                               (base 34153) with A in
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core: 92.000"
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70.000"
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/clone="ch19 cosmid f16632"
/replace="G in cosmid (base 34486) with
7341
                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLR
CRPVAVDVLLLNLTASDLLLLLFLPFRHVEAANGMHWPLPFILCPLSCBIFFTTTYLT
ALFLAAVSIERFLSVAHPLWYKTRPRLGAGLLVSVACWLLASAHCSVVYVIEFSGDIR
HSQGTMGTCYLEFWKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILIGRGGSHR
RQRRVAGLVAATLLNFLVCFGPYNVSHVVGYICGESPVWRIYVTLLSTLNSCVDPFVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLASTX similarity to P34976 (33. .68); match: 0.33, score: 2.4e-13; database searched: nr; TYPE-1 ANGIOTENSIN II RECEPTOR (AT1) pir||A48857 AT1 angiotensin II receptor rabbit >qi|299615 (S59041) AT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frame: 1, quality: marginal, score: 43.000"
complement(12401. 12451)
/note="predicted exon, program: grail?avona beframe: 2 amair."
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/clone="chi9 cosmid f16632"
/replace="insertion of -10 kb in complement(10667...1098)
/rpt_family="MER1"
                                                                                                                                                                                                                                                                                                                                                                       20319
                                                                                                                                                                                                                                                                                                                                                                                          YFSSSGFQADFHELLRRLCGLWGQWQQESSMELKEQKGGEEQRADRPAERKTSEHSQG
CGTGGQVACAEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"hypothetical 38 8 kDa protein similar to G-protein coupled receptors; BLASTX similarity to (16578) putative G protein coupled receptor (Homo sapiens); 9i1231669 (19323) purinergic receptor P2Y9 [Homo sapiens]; Pval-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11157. .11490)
/rpt_family="L1"
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7484. .19281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /replace="T in cosmid (base 35268) 7350
                                                                                                                                                                                                                                           21849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="PC28130_1"
/protein_id="AAB67885.1"
/db_xref="GI:2347083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality: excellent, score:
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                                                                                                                                                                                                                                                           /clone="ch19 cosmid f16632"
/replace="C in cosmid (base 36784) with
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13127. .13375
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/note="predicted exon, program:
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/clone="ch19 cosmid f16632"
                          'note="predicted exon,
                                                                                                                                                                           'standard_name="VNTR"
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                                                  . 23665
                                                                                                                                                                                               .22490
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predicted exon, program:
1, quality: good, score:
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2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon, program: grail2exons_human_1.3, frame: 1,
excellent, score: 93.000"
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C in cosmid (base 35277) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         m: grail2exons_human_1.3
score: 82.000"
    gra112exons_human_1.3
61.000"
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GGCGACAGAGACAGA-AATGAAACTCTGTCTCAAAAAACAAACAAACAAAAAAAA
                                                                          GAGAATCACTTGAATCCGGGAAGCAGAGATTGCAGTGAGCTGAGATTGCAGTCGAGCCTG
                                                                                                                       AATTTAGCTGGGCGTGGTGGCGGGCGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAG
                                                                                                                                       AAATTAGCTTGGCATGGTCGTGGGCACCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAG
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                                                          GAGGATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATCATACTACTGCACT
                                                                                                                                                                                TCAGGAGTTTCAGACCAGCCTGGCCAACATAGTGAAACCTCATCTCTACTAAAAATACAA
                                                                                                                                                                                                  AGATGACA - - - - TTTTATCCCTAAATACTTTAGA - - - - TAAAGGTGTTCTTTGAAAAAAA
                                                                                                                                                                                                                                                                                                         TTCTTTCGTGGAATGTCTGTTTAAATATTTTGCTCATTTAAAAAATTTTAGGCTGGGCAT
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24520. .24800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pseudo 28691. .
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/rpt_family="Alu"
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/rpt_family="Alu"
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frame: 2, quality: excellent, score: 81.000"
25659. .25928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted exon, frame: 1, quality: exce
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   core 225.6; DB 9 red. No. 3.5e-52; Mismatches 189
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/db_xref="family="MIR" /chromosome="17" /chromosome="17" /clone="18pk,786_O_4" /clone="lib="RPET-11 human BAC library" /clone=lib="RPET-11 human BAC library" /clone=lib="RPET-11 human BAC library" /clone=lib="RPET-11 human BAC library" /rpt_family="MIR"	Gage,D., Gardyna,S., Geraigery,K., Grant,G., Hagos,B., Heaford,A., Herrena,L., Horton,L., Howland,J.C., Jacotot,L., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., Meldrim,J., Molla,M., Morris,R., Morrow,J., Mychaleckyj,J., Nahf,R., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D., Ye,W.J., Zhao,J. and Zody,M. Direct Submission Submitted (11-NoV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 11, 1998 this sequence version replaced gi:3858905. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green,P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html. Location/Qualifiers 1. 172203 //oranisms*Homo.sanions**	Gage,D., Gardyna,S., Geraigery,K., Grant,G., Hagos,B., Heaford,A., Herena,L., Horton,L., Howland,J.C., Jacotot,L., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Maddonald,P., Marguis,N., McEwan,P., McGurk,A., McKernan,K., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Nahf,R., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,Y., Niloff,M., O'Connor,T., O'Donnell,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D., Ye,W.J., Zhao,J. and Zody,M. Direct Submission L Submitted (24-OCT-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 172203) Si Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C., Brown,A., Costle,A., Cerny,J., Collangelo,M., Collins,S., Donneln, L., Ferreitra, D., Fetringh, W., Devon,K., Dewar,K., Devon,K., Dewar,K., Devon,K., Dewar,K.,	AC005863 AC005863 AC005863 AC005863 AC005863.1 GI:3859654 HTG. HOMO sapiens. HOMO sapiens. Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 172203) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.786_O_4 Unpublished 2 (bases 1 to 172203) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Finke, R., Everest, C., Everest,
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Consensus quality: 417420 bases at least Q30
Consensus quality: 41761 bases at least Q20
Consensus quality: 41761 bases at least Q20
Estimated insert size: 62550; agarose-fp estimation
Estimated insert size: 43783; sum-of-contigs estimation
Quality coverage: 10.3 in Q20 bases; agarose-fp estimation
Quality coverage: 14.72 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 19 c.1
SEQUENCE, 5 unordered pieces.
ACO93229
                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-AUG-2001) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut------Genome Center
                                                                                                                                                                                                           Summary Statistics
                                                                                                                                                                                                                                              Center clone name: CITB-E1_3242E3
                                                                                                                                                                                                                                                               Project Information Center Project Name: 949056, BC914080
                                                                                                                                                                                                                                                                                                                                     Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                     Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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DOE Joint Genome Institute
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DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 GATTATAGGCGTGAGCCGCCGCCCAGCCAACA----TTTTTTAAATACTGAAAAGTAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 TAAGGCAAAACCCAGATGACATTTTATCCCTAAATACTTTAGATAAAGG---TGTTCTTT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TTTATTTCTTCTATACCAGTACCGTACTC------TCCCCACTGGGATTATTT 287
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1651: gap of unknown length
3140: contig of 1489 bp in length
3240: gap of unknown length
5838: contig of 2598 bp in length
5938: gap of unknown length
13301: contig of 7363 bp in length
13401: gap of unknown length
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Search completed: March 29, 2003, 21:04:04

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Sequence 10, Application US/09461474

Patent No. 6278042

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474

CURRENT FILING DATE: 1999-12-14

EARLIER APPLICATION NUMBER: 60/112,562

EARLIER FILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Microsoft Office 97

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                                               TL-HQSGHGHSHG----
                                                                 GFFRIEILGALVSIQLIWLLAGILVYEAIVRLINESGEVQGSLMFAVSAFGLFVNIIMAV
                                                                                                       IIAVILCIIFMAVEVVGGIKANSLAILTDAAHLLSDVAAFAISLFSLWAAGWEATPQQSY
                                                                                                                                             PKMDSHNSAPPQIAEVRMDISSSTSVAAGNKVCRGAACDFSDSSNSSKDARERMASMRKL
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                             LLGHDHGHGHGHGHGHSHDHDHGGSDHDHHHHEDQEHGHVHHHEDGHGNSITVNLHHH
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31.6%; Pred. No. 5.2¢
tive 72; Mismatches
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US-08-411-859-2
US-08-347-707-8
US-08-347-707-8
US-08-347-707-8
US-09-09-7-809-25
US-09-071-035-268
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US-09-071-035-262
US-09-071-035-263
US-09-071-035-263
US-09-173-281-9
US-09-173-281-9
US-09-134-001C-3935
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US-09-299-44-4
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US-09-610-417-4
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PCT-US95-10579-7
US-09-024-848-4
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DB 4;
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RESULT 3
US-09-661-474-17
Sequence 17, Application US/09461474
Patent No. 6278042
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
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GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB130 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 17
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US-09-461-474-8
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SEQ ID NO 8
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Best Local (
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GKVLLACHVTIARDADADEILDKVIGYIKTEYNISHVTIQVE
              AQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIE
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                                                           CTLVFSVVVLFTTIRMLRSILEVLMESTPREIDATRLESGLCGMEGVVAVHELHIWAITV
                                                                                          CTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTV
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Pred. No. 1.7e-64;
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; ORGANISM: Glycine max
US-09-461-474-12
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US-09-461-474-12
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: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-09-461-474-17
                                                                                                                                                                                                                                                                                                      APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
                                                                               Query Match 31.9
Best Local Similarity 37.2
Matches 128; Conservative
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SEQ ID NO 12
LENGTH: 349
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Patent No. 6278042
GENERAL INFORMATION:
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TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 17
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MIGEVVGGYLAHSLAVMTDAAHLLITDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGA 144
                                                                             31.9%; Score 613.5; DB 4; 37.2%; Pred. No. 2.2e-60; tive 62; Mismatches 81;
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                                                                                                                     Length 349;
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                                                                                 Indels
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	331 QAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQG 369 : : : : : : 296 QTCETMLKSIESDLL-QLNIQHMTIQLETPEHKHDESTLCSG 336	Db Oy	
)A 330 ;V 295	271 RDVILVLMEGTPKGVDETAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA : : : : : : : : : : : :	Qy dd	
IL 270 235	211 QEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTIL ::	Db Qy	
1Q 210 ·D 176	151 IWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQ ::::: :: : : : :	Оу	
LS 150 :: /T 126	91 GGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWORAEILGALVSVLS : : ::: ::: ::: ::: :::	Qy Db	
1 66 1 90	32 PLPRPGLDLQAIELAAQSNH-HCHAQKGPDSHCDPKKGKAQRQLYVASAICLLEMIGEVV	Qy da	
Gaps 7;	Query Match 21.2%; Score 408.5; DB 4; Length 342; Best Local Similarity 28.4%; Pred. No. 2.3e-37; Matches 97; Conservative 80; Mismatches 144; Indels 21;		
TO STAPHY	RESULT 5 US-09-134-001C-4190 US-09-134-001C-4190, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 4190 LENGTH: 342 TYPE: PRT ORGANISM: Staphylococcus epidermidis US-09-134-001C-4190	US	
	305 TVGKVLLACHVKIRREADADLVLDKVIDYIKRVYNISHVTIQIE 348	da	
	312 TVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIE 355	Оу	
	4	Db 2	
	50 0	Qy (
7D 251	206GTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVD	η Q	
1A 184	125 AGHSHGHGHGHSHGFTMSTHCDAKHTKDQНННТНННDENHPKDAHHHTDEDHLНННА	Db	
205	199SGHGHSH	Qy	
2- 198 RH 124	145 LVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQ- : : : : : :	Qy Db	

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APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER TLING DATE: 1998-12-16
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5618
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                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09461474 Patent No. 6278042
                                                          SEQ ID NO 14
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PRIOR FILING DATE: 1997-11-08
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                                                                             SOFTWARE: Microsoft Office 97
                                                                                                  NUMBER OF SEQ ID NOS:
                    LENGTH: 157
TYPE: PRT
ORGANISM: Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 NRRIHAWRRDMENKPDYFHHIEHRKFQSSSKITLWLSLVITMIFTVVEFVGGIVSNSLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLQGKFHFHTVTIQIED 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQN--TDAQAVLKTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWHFIGDLLNSLGIIVAFVLIHF-TGWNIVDPIISILISLIILRGGYKIIKNASKVLMER
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Pred. No. 1.1e-34;
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US-09-134-001C-2867; Sequence 2867, Application US/09134001C; Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: UNSURE ; LOCATION: (157) ; OTHER INFORMATION: Identity of amino acid at the above locations US-09-134-001C-2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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APPLICANT: LYNN DOUGETLE-Stamm et al
APPLICANT: LYNN DOUGETLE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                              Sequence 520, Application US/08858207A Patent No. 6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2867
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 167
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                    APPLICANT: Black, Michael APPLICANT: Hodgson, John APPLICANT: Knowles, David APPLICANT: Nicholas, Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
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                                                                                                                                                                                                                                                                                                  336 TASSRLQGKFHFHTVTIQIE 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.9 es 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVIL 275
                                                                                                                                                                                                                                                                                                                                       FLMEGVPLHIDYIVVGTDVDQVDGVIAVHDLHVWDMSPGQPALIGHVEIEHLDHWPNVLR 122
                                                                                                                                                                                                                                                                                                                                                                                                                STRAALVHVMGDLLGSVAGIIAGAVIYC-TGWMQIDPLLSVLVSLLILKSTFGVLRESYH 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                         Hodgson, John
Knowles, David
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43.0%;
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Pred. No. 1.:
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Pred. No. 2e-30;
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STREET: 709 SwedeLand CITY: King of Prussia

ADDRESSEE: SmithKline STREET: 709 Swedeland

Beecham Corporation

Road

COUNTRY: USA ZIP: 19406-0939

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US-09-134-001C-3700
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lynn Dou
                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 3700
LENGTH: 154
                                                                                                                                                                                                                                                                                                                        Sequence 3700, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                          PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
ORGANISM: Staphylococcus epidermidis FEATURE:
                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     123 INLLASLVV---GKG------KTKNESILS--LHFLEDTLGWVAVILMAIV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 TKTMNFGWQRAEILGALVSVLSIWVVTG-VLVYLAVERLISGDYEIDGGTMLITSGCAVA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 KAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLIDFASMLISLFSLWMSSRPA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 DNQYTLGYKRFSLLGALVT--AVILVTGSVLVILENVTKILHPQPVNDEGILWLGIIAIT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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14-MAY-1996
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27.2%;
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Pred. No. 2.3e-06;
Pred. No. 2.3e-71;
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32 PLPRPGLDLQAIELAAQSNHHCHA--QKGPDSHCDPKKGKAQRQLYVA-----SAICLLF

Matches

Similarity

Conservative

137;

Indels

113;

Gaps

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; NAME/KEY: UNGURE; LOCATION: (109),(135),(143); LOCATION: INFORMATION: Identity of amino acid at the above locations are unknown US-09-134-001C-3700
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              Query Match
Best Local S
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                     TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-MAR-19;
CLASSIFICATION: 435
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EVANS, CHRISTOP APPLICANT: KEITH, DUANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FITLE OF INVENTION:
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                                                                            LOCATION: group(18, 33)
OTHER INFORMATION: /note= "extracellular Asn residues
OTHER INFORMATION: that are consensus sites for N-linked glycosylation"
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                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                 amino acid
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21.6%;
5.2%; Score 100.5; D
21.2%; Pred. No. 0.01;
tive 59; Mismatches
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Pred. No. 0.0026;
""Fmatches 56;
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                               DB 4;
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US-09-134-001C-5241
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5241
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APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: DIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT TELLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5241, Application US/09134001C Patent No. 6380370
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Best Local Similarity
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                                    T--AVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKF
                                                                             LIQSLGVFFDTML-----
                                                                                                               FMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDF
                                                                                                                                                        GVQQVTGGAV----GAAILQGIKRGLFSNEAGMGSA-----PNAAATSAVPHPVKQG
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                                                                                                                                                                                                                                                                                                                                                                                             61;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 88; DB 4; Length 489; Pred. No. 0.4; 53; Mismatches 119; Indels
                                                                           ----VCT-----ATAIMILLYSGLQFGDSAPQGVAV
-FLTVAVTLFAFSSVVGNYYYGQSNIEFLSNNKMILF
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LENGTH: 766

TYPE: PRT

ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3689
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US-09-268-866-2
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US-09-134-001C-3689
                                  SOFTWARE: Pate
SEQ ID NO 2
LENGTH: 1212
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Mack, D
                                                                                                                                                                                                                                                                                                                Sequence 2, Application Patent No. 6316272
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                                                                                         APPLICANT: Gish, Kurt C.
APPLICANT: Wilson, Keith E.
APPLICANT: Wilson, Keith E.
TITLE OF INVENTION: No. 6316272el Methods of Diagnosing of Colorectal Cancer,
TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
TITLE OF INVENTION: Cancer Modulators
FILE REFERENCE: A67474/RMS/DAV/JUD
CURRENT APPLICATION NUMBER: US/09/268,866
CURRENT FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
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TYPE: PRT ORGANISM:
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les 61; Conserv
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                                                                                                                                                                                                                               : Mack, David
: Gish, Kurt C.
: Wilson, Keith I
Homo
                                                                           PatentIn Ver. 2.0
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21.2%; Pred. No. 1.2;
tive 50; Mismatches
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APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Sirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT EILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 7257

TYPE: PRT

ORGANISM: Sorangium cellulosum

US-09-335-409-5
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Best Local Similarity 22.6
Matches 48; Conservative
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1190 WGRDQPPEVRARIAAIEALEAQGARVTVAA----
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                                                                                    ----ENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLT 268
                                                                                                                                                                                                                                                                                                                  ----MSSRPATKTMNFGWQRAEILGALVSVLS-----IWVVT------ 155
                                                                                                                                                                                                                         ------GVLVYL-----AVERLISGDYEID------
                                                                                                                               ----GGTMLITSGCAVAVNIIMGLTLHQSGHGH-----SHGTTNQQE 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 126;
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                                                 GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Lipon, James
APPLICANT: Molnar, Istvan
APPLICANT: Mikle, Ross
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LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
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                                                                                                                                                       Sequence 5, Application US/09568480 Patent No. 6355458
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APPLICANT: Ligon,
APPLICANT: Molnar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver.
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                                       APPLICANT:
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CANT: Goerlach, Joern
OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
                                                                                                                                                                                                                                                                           DDGLLAHQDAGRLARVLRPKVEGAWVLHTLT 1280
                                                                                                                                                                                                                                                                                                              ---IAQNTDAQAVLKTASSRLQGKFHFHTVT 351
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Molnar, Istvan
Zirkle, Ross
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                                     Cyr, Devon
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18.6%; Pred. No. 54;
18.6%; Mismatches 126;
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US-09-568-486-5
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                                                                                                                                                                                                                                                                                                                                               Sequence 5, application US/09568486 Patent No. 6355459 GENERAL INFORMATION:
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                                                   SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 4-30802A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
                                                                                           CURRENT APPLICATION NUMBER: US/09/568,486 CURRENT FILING DATE: 2000-05-10 PRIOR APPLICATION NUMBER: 09/335,409 PRIOR FILING DATE: 1999-06-17 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                            APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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TYPE: PRT
ORGANISM: Sorangium cellulosum
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                                                                         SOFTWARE: PatentIn Ver. 2.0
ORGANISM: Sorangium cellulosum
                     TYPE: PRT
                                     LENGTH: 7257
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                                                                                                                                                                                                                                                                     Molnar, Istvan
Zirkle, Ross
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18.6%;
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Pred. No. 5
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CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-472-5
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                                                                                                                                      Query Match 4.4
Best Local Similarity 18.6
Matches 84; Conservative
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Best Local Similarity
Matches 84; Conserv
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APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: 21rkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
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                                           902 WQRQRYWIEAPAEGLGATAADALAQWFYRVDWPEMPRSSVDSRRARSGGWLVLADR---- 957
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84 FMIGEVVGGYLA------HSLAVMTDAAHLLT-----DFASMLISLFSLW----- 122
                                                                                    WQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLL 83
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                                                                                                                                                            4.4%; Score 85.5; 18.6%; Pred. No. 54;
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18.6%; Pred. No. 54;
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                                                                                                                                        46; Mismatches 126;
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                                                                                                                                                                                    DB 4; Length 7257;
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                                                                                                                                        Indels 195;
                                                                                                                                      Gaps
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	Db 958 GGVGEAAAAALSSQGCSCAVLHAPAEASAVAEQVTQALGGRNDWQGVLYLWGLDAV 1013	
19;	Qy 123MSSRPATKTMNFGWQRAEILGALVSVLSIWVVT 155	
	-ALIQALGTGPRSPR	
	Qy 156	
	Db 1071 AALWGWGRVAALEHPGSWGGLVDLDPEESPTEVEALVAELLSPDAEDQLAFRQGRRRAAR 1130	
	Qy 175	
	Db 1131 LVAAPPEGNAAPVSLSAEGSYLVTGGLG-ALGLLVARWLVERGAGHLVLISRHGLPDREE 1189	
	Qy 213ENPSVRAAFIHVIGDEMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLT 268	
	Db 1190 WGRDQPPEYRARIAAIEALEAQGARVTVAA	
	QY 269 ILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIA 323	
	Db 1220VDVADAEGMAALLAAVEPPLRGVVHAAGLL 1249	
	KFHF	
	Db 1250 DDGLLAHQDAGRLARVLRPKVEGAWVLHTLT 1280	
	RESULT 21 US-09-567-899-5	
	6383787 ORMATION:	
	; APPLICANT: Ligon, James	
	; APPLICANT: Zirkle, ROSS ; APPLICANT: Cyr, Devon	
	; APPLICANT: GOETLACH, JOERN ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES : FTLE REFERENCE: 4-30582A	
	CIPE DEFENDE: 4 303048 CURRENT APPLICATION NUMBER: US/09/567,899 CURRENT FILING DATE: 2000-05-10 PRIOR APPLICATION NUMBER: 09/335,409	
	FILING DATE: 1999-0 R OF SEQ ID NOS: 30 ARE: PatentIn Ver. 2	
	; SEQ ID NO 5; ; LENGTH: 7257 ; TYPE: PRT ; ORGANISM: Sorangium cellulosum US-09-567-899-5	
	Query Match 4.4%; Score 85.5; DB 4; Length 7257; Best Local Similarity 18.6%; Pred. No. 54; Matches 84. Conservative 46. Mismatches 126. Indels 185. Gans 10.	
	AQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLL 83	
	Db 902 WQRQRYWIEAPAEGLGATAADALAQWFYRVDWPEMPRSSVDSRRARSGGWLVLADR 957	
	84	
	Db 958 GGVGEAAAALSSQGCSCAVLHAPAEASAVAEQVTQALGGRNDWQGVLYLWGLDAV 1013	
19;	123MSSRPATKTMNFGWQRAEILGALVSVLSIWVVT	
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	Db 1071 AALMGMGRVAALEHPGSWGGLVDLDPEESPTEVEALVAELLSPDAEDQLAFRQGRRRAAR 1130	
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US-08-993-088A-7
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                                                                                                                      Best Local Similarity 22.8 Matches 46; Conservative
                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 387 amino acid
                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lin-
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
TITLE OF INVENTION: NUCLECTIDES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: UDDATE STATES
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                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                 82 LLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISL-----FSLMMSSRPATKTMNFG 135
                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/993,088A FILING DATE: 18-DEC-1997 CLASSIFICATION: 530
                                                      34
                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179 REFERENCE/DOCKET NUMBER: 19846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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WQRAEILGALVS-----VLSIWVVTGVLYYLAVERLISGDYEIDGGTMLITSGCAVAV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLS--VHIA--- 323
                                                 LIFLYG-TYGNTLY--LAVLLRGGQAYSTTNLFILNLGYADLCFILCCYPFQATIYTLDG 90
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P.O. Box 2000, 126 E. Lincoln Ave
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SYSTEM: Windows
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US-08-750-723A-2
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REFERENCE/DOCKET NUMBER: GETELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (212) 596-9000
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NAME: James F. Haley, Jr., I
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 15-JUN-1994
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186 AMD-ICTFVFSYLLPVLVLGLT 206
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                                                                                                                                  389 AVTAAILGLSVLLİTGVVTWKECLAESVAWDTLTWFAALIAMAGYLNKYGLITWFSEN--
                                                                                                                                                                    184 -----CAVAVNIIMGLT----
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493 VASAL--GTP 500
                                273 VILVLMEGTP 282
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: New York
STATE: New York
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ZIP: 10020
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                                                                ----VVKVVGGLGLSWQMSFGVLV---LLYFYSHY--
                                                                                                  VRAAFIHVIG----DFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber, Andreas
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Pred. No. 1
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                                                                  --FFASGAAHIGAMFTAFLS
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US-09-191-275-2
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: James F. Haley, Jr.,
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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1251 Avenue of the
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TELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: RObinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: HULMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                          199
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                                                                                                                                                                                                                              114 WPFGELLCKAVLSIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIW 173
                                                                                                                                                                                                                                                                   136 WQRAEIL-GALVSV-----LSIWVVTGVLV--YLAVERLISG-DYEIDGGTMLI----- 180
                                   290 VRDLLLSVEG--VEALHSLHI----WALTVAQ-----PVLSVHIAIAQNTDAQAVLKTAS 338
                                                                                                                                                                                        181 --TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAA 238
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                                                                                                                                                                                                                                                                                                        63 GLLGNVL-----VMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMET 113
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                                                                                                                                                     VLASGVGVPI-MVMAVTQPRDG------
                                                                                                            YILYFKPEYKY--VDPICTFVFSILVLGTTLTILRDVILV-----LMEGT-PKGVDFTA 289
ITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIA-----LGYAN
                                                                          TLQFPSPSWYWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRR
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805 Third Avenue
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; Pred. No. 0.8;
59; Mismatches
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US-08-454-552-4
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Best Local
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TELEX: 236687
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 367 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rat
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VLASGVGVPI-MVMAVTQPRDG----
                                                                              --TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAA 238
                                                                                                               WPFGELLCKAVLSIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIW 173
                                                                                                                                              WORAEIL-GALVSV-----LSIWVVTGVLV--YLAVERLISG-DYEIDGGTMLI----- 180
                                                                                                                                                                                                                   FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNF------G 135
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HULMES, Jeffrey D.
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                                                      ---AVVC
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TITLE OF INVENTION: COMAS ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
FILE REFERENCE: 0646/LA818US1
CURRENT APPLICATION NUMBER: US/08/676,351C
CURRENT FILING DATE: 1996-09-12
EARLIER APPLICATION NUMBER: PCT/US95/00939
EARLIER FILING DATE: 1995-01-20
EARLIER FILING DATE: 1995-01-20
EARLIER APPLICATION NUMBER: US 08/185,360
EARLIER FILING DATE: 1994-01-21
NUMBER OF SEQ ID NOS: 11
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 367
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; TYPE: PRT
; ORGANISM: Rat
US-08-676-351-3
RESULT 29
US-08-188-275A-4
; Sequence 4, Application US/08188275A
; Patent No. 6258556
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US-08-676-351-3
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Best Local Similarity 20.6
Matches 81; Conservative
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APPLICANT: EPPLER, CECIL
APPLICANT: OZENBERGER, BRADLEY
APPLICANT: HULMES, JEFFREY
APPLICANT: HULMES, JEFFREY
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                                                                                                                                     311 SSLN------PVLYAFLDENFKRCFRQLCRAP 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 83.5; DB 3; Length 367; 20.6%; Pred. No. 0.82; ative 59; Mismatches 139; Indels 11
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Qy	Db	Qy	Db	Qу	Db	Qy	ДD	Qу	фa	Qy		US.				·. ·. ·	·· ··			·. ·.						·. ·.			٠. ٠			• ••						
290 VRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIATAQNTDAQAVLKTAS 338	199 TLQFPSPSWYWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRR 258	239	174 VLASGVGVPI-MVMA	181		136	63 GLIGNVLVMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMET 113	84 FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATK	ω	32	Query Match 4.3%; Score 83.5; DB 4; Length 372; Best Local Similarity 20.6%; Pred. No. 0.84; Matches 81; Conservative 59; Mismatches 139; Indels 115; Gaps 20;	OTHER INFORMATION: /note= "rat delta opiate receptor"	. F10CE111 : 1372 : 7372 /label=	FV. Dr	멀	STRANDEDNESS: double TOPOLOGY: linear	TYPE: amino acid	SEQUENCE CHARACTERISTICS:	_	TELEPHONE: 703-241-1300 TELEPAX: 703-241-2848	ATION INFORMATION:	REGISTRATION NUMBER: 28,977	ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald M.	CLASSIFICATION: 530	APPLICATION NUMBER: US/08/188,275A FILING DATE: 28-TAN-1994	SUFTWARE: FACENCIN RELEASE #1.0, VEISION #1.25 CURRENT APPLICATION DATA:	TEM: PC-DOS/MS-DOS	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	COMPUTER READABLE FORM:	COUNTRY: USA	CIII: FallS Church STATE: Virginia	P.O. Box 747	CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Stewart, Kolasch & Birch	R OF SEQUENCES: 12	NVENTION:	APPLICANT: Johnson, Peter S. APPLICANT: Persico, Antonio	Wang, Jia-Bei	GENERAL INFORMATION: APPLICANT: IIbl. George R.

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; APPLICANT: Yu, Lei
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALELES OFTHE HUMAN MU OPIOID RECEPTOR, DIA
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS
; TITLE OF INVENTION: BASED THEREON
; TILE REFERENCE: 600-1-226N
; CURRENT FAPPLICATION NUMBER: US/09/351,198
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
  TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-351-198-4
                                                                                                                               RESULT 31
US-09-113-426-4
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US-09-351-198-4
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                                                                 GENERAL INFORMATION:
                                                                                      Sequence 4, Application US/09113426 Patent No. 6337207
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Best Local :
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APPLICANT: Kreek, Mary J
APPLICANT: Laforge, Karl
APPLICANT: Yu, Lei
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APPLICANT: Laforge, Karl
APPLICANT: Yu, Lei
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Local Similarity 20.6%; Pred. No. 0.84;
nes 81; Conservative 59; Mismatches 139; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNF------G 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKG-KAQRQLYVA-----SAICLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PVPSARAELQFSLLANVSDTFPSAFPSASANASGSPGARSASSLALAIAITALYSAVCAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLASGVGVPI-MVMAVTQPRDG---
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                                                                                                                                                                                                                        SSLN------PVLYAFLDENFKRCFRQLCRAP 336
                                                                                                                                                                                                                                                     SRLQGKFHFHTVTIQIEDYSEDMKDC--QACQGP 370
                                                                                                                                                                                                                                                                                                          ITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIA-
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                                                                                                                                                                                                                                                                                                                                                                                              TLQFPSPSWYWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRR 258
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (99)
; OTHER INFORMATION: X
US-09-369-364A-22
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US-09-369-364A-22
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Best Local S
Matches 81
                                                                                                                                                                            SOFTWARE: 1
SEQ ID NO 22
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SEQ ID NO 4
LENGTH: 372
TYPE: PRT
ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09369364A Patent No. 6391610
                                                                                                                                                                                                                     APPLICANT: Hurskainen, Tilma L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILLMG DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: ALELES OFTHE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
TITLE OF INVENTION: BASED THEREON
FILE REFERENCE: 600-1-226
                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                         LENGTH: 518
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                                                                                                                                                                                                       PatentIn
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20.6%; Pred. No. 0.84;
tive 59; Mismatches 139;
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Query Match

4.3%;

Score 83.5;

DB 4;

Length 518;

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US-09-122-126B-15
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US-08-560-005-6
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Best Local S
Matches 50
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
                                                                                                                                                                            Sequence 6, Application US/08560005 Patent No. 6001354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENCTH: 930
TYPE: PRT
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                                                                                                                                                            GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 21
                                    APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating
TITLE OF INVENTION: Acids Encoding Therefor
                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                  330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 22.4 les 50; Conservative
            ADDRESSEE:
                                                                                                                                                                                                                                                                                  T----
                                                                                                                                                                                                                                                                                                                AQAVLKTASSRLQGKFHFHTVTIQIEDYSEDM-KDCQACQGPS 371
                                                                                                                                                                                                                                                                                                                                                   YSFFVPKKSTPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                    PSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDV- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRFTAYLALKKK-NGEYLINGKYMISTSETIIDIN---GTVMNYSGWSHR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEEN 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRFTAYLALKKK-NGEYLINGKYMISTSETIIDIN---GTVMNYSGWSHR------
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                                                                                                                                                                                                                                                                                ------GWHTRTVQCQDGNRKLAKGCPLSQRPS 920
          Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GWHTRTVQCQDGNRKLAKGCPLSQRPS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.4%; Pred. No. 1.4;
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22.4%; Pred. No. 3.6;
tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                ----VNSVTSHGSNKVGSHT-SQPQWVTGPWLACSRTCD
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                                                                         Protein and Nucleic
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Best Local Similarity
Watches 51; Conserve
                                                                                                                                                                                                                             US-09-418-540-6
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                                                                                                                                                                                                                                             RESULT 35
                                                                                                                                                                                          Sequence 6, Application US/09418540 Patent No. 6296848
APPLICANT: Pot, David...

APPLICANT: Williams, Lewis T.

APPLICANT: Wefferson, Anne Bennett

APPLICANT: Majerus, Philip W.

TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic

TITLE OF INVENTION: Acids Encoding Therefor

NUMBER OF SEQUENCES: 10

NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                455
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ZIP: 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                              Q 455
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                                                                                                                                                                                                                                                                                                                                                                 AETVGTGIMGRMGNKGGVAIRFQFHNTSICVVNSHLAAHIEEYERRNQDYKDICSRMQFC
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                                                                                                                                                                            INFORMATION:
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Pred. No. 4.1;
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                                                                                                                                                   Sequence 2, Application US/08362512A Patent No. 5719043
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Best Local S
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 anino acids
                                                                                                                                     GENERAL INFORMATION:
                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
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TELEPHONE: 415-326-2400
                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 23
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TOPOLOGY: linear
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                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                        AETVGTGIMGRMGNKGGVAIRFQFHNTSICVVNSHLAAHIEEYERRNQDYKDICSRMQFC
                                                                                                                                                                                                                                                                                                                                                       AQAVLKTASSRLQGK-----FHFHTVTI-----QIEDY---SEDMKD----CQAC
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: California
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E: Ostrolenk, Faber, Gerb & 1180 Avenue of the Americas
                                                                                   FROMMER, WOIf-Bernd
NVENTION: DNA SEQUENCES FOR AN AMINO ACID
NVENTION: TRANSPORTER, PLASMIDS, BACTERIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                   CONTAINING A TRANSPORTER AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 83; DB 4; Length 942; 21.2%; Pred. No. 4.1;
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               Gerb & Soffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
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US-08-964-939-2
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Best Local Similarity 18.1
Matches 63; Conservative
                                                                                                                                               Sequence 2, Application US/08964939 Patent No. 6245970
                                                  GENERAL INFORMATION:
APPLICANT: FROMMER, WOLF-BEIDD
TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA,
TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/007,636
FILING DATE: 21-JAN-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P/951-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
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MEDIUM TYPE: Floppy disk
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LENGTH: 485 amino acids
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                   CORRESPONDENCE ADDRESS
                                  NUMBER OF SEQUENCES:
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ADDRESSEE:
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Faber, Gerb & Soffen
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Pred. No. 1.7;
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GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                   Sequence 3703, Application US/09134001C Patent No. 6380370
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,512
FILING DATE: 05-JAN-1995
APPLICATION NUMBER: US 08/007,636
FILING DATE: 21-JAN-1993
ATTORNEY/AGENT INFORMATION:
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LENGTH: 485 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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SOFTWARE: PatentIn Release #1.0,
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REFERENCE/DOCKET NUMBER: P/951-107
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Pred. No. 1
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LENGTH: 496
TYPE: PRT
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SEQ ID NO 5457
LENGTH: 524
TYPE: PRT
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local :
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-11-08
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                                        102 SEKLGNPK--SGDIILKGSDILGTNNALSHAFSGFSTSAVALVAAALFLA-----VA 151
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                                                                                  158 LVYLAVERLISGDYEIDGGTMLIT-----
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QQEENPSVRAAF--IHVIGDFMQSM---GVLVAAYILYFKPEYKYVDPICTFVFSILVLG 264
                                                                                                                                                                  LAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGV 157
                                                                                                                                                                                                              ETIKMAKGDQYQAHTEK----YHDKKSKKSYKPVWIIISFIILITILLLPTPAG-----
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                                                                                                                          LPVMAKAALAILAFAVV-----MWV-----TEAVTYPVSATLILGLMILLLGLSPVQDL 101
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                                                                                                                                                                                                                                                                                                 Score 82.5; DI
Pred. No. 1.9;
62; Mismatches
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US-08-484-840-2
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Best Local S
Matches 58
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,840
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
DEPERATOR OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08484840 Patent No. 5716788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: MOSCOW
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APPLICANT: DIXON, Kathy
APPLICANT: HE RUI
APPLICANT: HE RUI
TITLE OF INVENTION: A GENE ENCODING A HUMAN REDUCED FOLATE
TITLE OF INVENTION: CARRIER (RFC) AND METHODS FOR THE TREATMENT OF
TITLE OF INVENTION: METHOTREXATE-RESISTANT, TRANSPORT-DEFICIENT CANCER CELLS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 40399/324/NIHD TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
325 GFVKIRWARWSKLLIAGVTATQAG--
                                                                  186 VAVNI-----IMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLV 236
                                                                                                                                                                                                                      144 ALVSVLSIWVVTGVLVYLAV-----
                                                                                                                                                                                                                                                                                                235 GGKLGHALRVACGDSVLARMLRELGDSLRRPQLRLWSLW----- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 TTLTILRDVILVLMEGTPKGVDFTAVRD-LLLSVEGVEALHSLHIWALTV----AQPVLS 319 : | | : : | : : | : : | | : ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 MQETNLHKRLALLVLSIVGNKTRNIVIGAILVSIVLAFFVPS------ATARAG
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                                                                                                                                                                                                                                                                                                                                                                      91 GGYLAHSLAVM----TDAAHLLTDFASML----ISLFSLWMSSRPATKTMNFGWQRAEILG 143
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                                                                                                                                            WVFNSAGYYLVVYYVHILWNEVDPTTNSARVYNGAADA-ASTLLGAITSFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%; Score 82.5; DB 1; Length 591; 21.6%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Mismatches
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                                                                                                                                                                                                          ----ERLISGDYEIDGGTML--ITSGCA 185
-----LVFLLAHTRHPSSIWLCY 366
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Search completed: March 18, 2003, 15:42:48
Job time: 37 secs

Q947r8 eucalyptus Q8t0g1 drosophila Q9m271 arabidopsis Q9w9i1 drosophila

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Title:
Perfect score:
Sequence:
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Maximum DB s
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Q9RMF3
Q95QW4
Q18009
Q9VGS1
Q8TDG3
L Q9JKN1
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Q9H9X0
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Q9JKN2
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0 Q94911
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0 Q94886
    Q8ZUMO
Q9NPWO
069597
Q9CCX3
Q97K27
Q92PO3
Q94GQ3
P93574
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Q9zw23 arabidopsis
Q8sqt3 encephalito.
Q9pf12 xylella fas
Q9x7q7 streptowyce
Q8y480 listeria in
Q9r494 bacillus st
Q9x781 listeria me
Q927r8 dacillus st
Q99sb4 staphylococ
Q9znf5 staphylococ
Q9znf5 staphylococ
Q9znf6 staphylococ
Q9zr4 drosophila
Q9bb67 caulobacter
Q9bz76 homo sapien
Q9bz76 homo sapien
Q9rv7 deinococus
Q9rv77 deinococus
Q9732 clostridium
Q9prv7 deinococus
Q9732 clostridium
Q9prv7 deinococus
Q9rs18 aquifex aeo
Q9732 clostridium
Q9yac08 thermotoga
Q9si03 arabidopsis
Q8zsal anabaena sp
Q8us08 caenorhabdi
Q9fx12 mus musculu
Q8r4f9 mus musculu
Q8r4f9 mus musculu
Q8r4f9 homo sapien
Q9fx62 caenorhabdi
Q9fx12 drosophila
Q8td3 homo sapien
Q9cf74 lactococcus
Q9cf74 lactococcus
Q9cf74 lactococcus
Q9tx18 anabaena sp
Q9fx65 streptococc
Q8yt81 anabaena sp
Q9fx65 streptococc
Q9yr82 drosophila
Q9cf82 prosophila
Q9cf83 prosophila
Q9cf847 pseudomonas
Q9fx65 streptococc
Q8yy5 drosophila
Q9cf83 drosophila
Q9cf83 drosophila
Q9cf84 streptococc
Q9xy65 streptococc
Q9x968 streptococc
Q9x968 streptococc
Q9x968 streptococc

Q8zum0 pyrobaculum
Q9npw0 homo sapien
069597 mycobacteri
Q9ccx3 mycobacteri
Q97k27 clostridium
Q92p03 rhizobium m
Q9hgq3 schizosacch
P93574 solanum tub

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RESULT 1
Q9BRI3
ID Q9BR
AC Q9BR
DT 01-J
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DT 01-J
DT 01-J
DT 01-J
DT 11-J
DT 11-
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Q9BRI3;
O1-JUN-2001 (TrEMBLrel. 17, C:
O1-JUN-2002 (TrEMBLrel. 21, L:
O1-JUN-2002 (TrEMBLrel. 21, L:
Similar to Zink transporter 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databuser
EMBL; BC006251; AAH06251.1; -
Interpro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
TIGRFAMS; TIGR01297; CDF; 1.
TIGRFAMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-OVARY;
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                                                    SHCDPKKGKAQRQLYVASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDEASMLISLES
LWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLI
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Q8TT22
6 Q8Y545
6 Q9P06
7 Q9P06
7 Q9P85
9 Q9R85
6 Q9R85
6 Q9R85
8 Q9H85
8 P7888
9 P7808
9 P72068
9 Q8T188
9 Q8T188
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9 P96NC3
0 RXMT3
0 RXMT3
0 RXMT3
0 RXMT2
0 RX
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Pred. No. 1.6e
0; Mismatches
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O8tkn5 methanosarc
O96yr3 sulfolobus
O9knp1 vibrio chol
O8xvq7 ralstonia s
O8tt22 methanosarc
O8y545 listeria mo
O9hp06 halobacteri
O9rh59 bradyrhizob
O92815 listeria in
O8rey6 fusobacteri
O9rh59 bradyrhizob
O92815 clostridium
P72068 nannocystis
O8tt88 methanosarc
O929e4 listeria in
O229e4 methanosarc
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08r42 mus musculu

09ruz4 deinococcus

082250 arabidopsis

09213 staphylococ

08y414 listeria mo

030282 archaeoglob
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Q96nc3 homo sapie
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RESULT
Q8TCL3
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AC Q8
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Best Local S
Matches 189
Q8TCL3;
Q8TCL3;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-TESTIS;
Strausberg R.;
Strausberg R.;
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases
SMBL; BC028358; AAH28358.1; -.
EMBL; BC028358; AAH28358.1; -.
SEQUENCE 388 AA; 41945 MW; D73DE65F46860FD8 CRC64;
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OBTCO3;
OBTCO3;
OBTCO3;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Solute carrier family 30 (zinc transporter), member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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mes 189; Conservative
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                                                                                                                       YAPLEEGPEEPLPLGNTSVRAAFVHVLGDLLQSFGVLAASILIVFKPQYKAADPISTFLF
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 (TrEMBLrel.
                       PRELIMINARY;
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53.7%;
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REDLINE-BERKELEY;

RX MEDLINE-20196006; PubMed=10731132;

RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D. (Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Rallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Rallew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
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Q9V471;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence upda
O1-JUN-2002 (TrEMBLrel. 21, Last annotation up
BG:DS07295.1 protein (RE54080p).
BG:DS07295.1 OR CG3994.
BG:DS07295.1 OR CG3994.
SDrosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
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Mammalia; Eutheria;
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SEQUENCE 37
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RRA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Dodson K.J., Evanqelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeed M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rahert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yelli X., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,
RA Yelli X., Yeng E.W., Rubin G.M., Venter J.C.,
The Yer R., Shith H.O.
The Globe Sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
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Celniker S., Rubin G.M.;
"An exploration of the sequence c
Drosophila melanogaster: the Adh
Genetics 153:179-219(1999).
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STRAIN-BERKELEY;
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L., Rubin G.M.;
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arris N., Hartzell G., Harvey D.,
Johnson G., Martin C., Moshrefi A.,
ing A., Tsang G., Wan K., Whitelaw K
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Eukaryota; Metazoa; Ner
Rhabditidae; Peloderina
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01-NOV-1996 (TrEMBLrel.
                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z68119; CAA92193.1; -.
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NHHCHAQ-KGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLL 108
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                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                           Peloderinae;
                                                                                                                                                                             PubMed=9851916;
                                                                                                                                                                                                                                                            Nematoda; Chromadorea; cinae; Caenorhabditis.
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                                                 Score 838.5;
Pred. No. 6e
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4; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                44A02AEF60B89484
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                        382
                                                  6e-64;
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                                                           DB 5;
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                                       93;
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           RA Ballew R. M. Basu A. Baxendale J., Buyraktaroğlu L., Beasley E.M.,
RA Beesen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beesen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beesen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guban P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA William S. M. Woodace T. Win C. Will D., Vang S., Van O. A.
  Wang Z.-Y
Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeilfer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Aphayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B.W., Brands B.W., Brandson C.R., Baldwin D.,
Ballow B.W., Brandson B.W., Brandson C.R., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Pterygota; Neoptera; Ephydroidea; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
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01-MAY-2000
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Metazoa; Arthropoda; Tracheata; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
a; Drosophilidae; Drosophila.
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  Yao Q.A.,
                                                                                                                                                                                                                                                                                                  K.A.,
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Best Local
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R EMBL; AE003635; AAF53175.1; -
R FlyBase; FBgn0032418; CG17215.
R FlyBase; FBgn0032418; CG17215.
R InterPro; IPR000357; CG17215.
R InterPro; IPR000357; CG2CR_Mgr.
R InterPro; IPR000337; GPCR_Mgr.
R InterPro; IPR000834; TGREN_Mgr.
R InterPro; IPR000839; CDE; 1.
R TIGREAMS; TIGR01297; CDF; 1.
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OBTC39;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
501ute carrier family 30 (zinc transporter), member
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101
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PROSITE: PS50259; G_PROTEIN_RECEP_F3_4; 1.
SEQUENCE 1677 AA; 188028 MW; F50ABD28ZA8E3B6E
Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC026089; AAH26089.1; -. SEQUENCE 429 AA; 47482 MW; 97B7FCBE881C8C32 CRC64;
                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                             TISSUE-TESTIS;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTEVFSILVLGTTLTILR
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                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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.ches 114;
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Smith
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Best Local
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045923;
01-JUN-1998 (TEMBLIEL 06, C:
01-JUN-1998 (TEMBLIEL 06, L
01-JUN-2002 (TEMBLIEL 21, L
Y39E4A.2b protein.
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                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALD21480; CAAL6328.1; -.
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TICRFAMS; TICR01297; CDF; 1.
SEQUENCE 410 AA; 44082 MW; 8379EA
                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                          none;
                                                                                                                                                                                                                                     MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                     Barlow
                                                                                                                                                                                                    "Genome sequence of the nematode investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402
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            95
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DYIKEALMKIEDVYSVEDLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLQGKF ::: |: :| |: | |: | | |
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                                 HSHTHNNDDSSSDCSGAGGGAHKHSHDEKYQKGRRAEKVLWAVAALSAVFIAAEFVGGFW 125
                                                        HCHAQKGPDSHCD------
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                                                                                al Similarity
139; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
                                                                            Score 709.5; DB 5;
Pred. No. 8.2e-53;
3; Mismatches 104;
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Pred. No. 6.6e-54;
8; Mismatches 117;
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on update)
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Best Local
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Science 282:2012-2018(1998).
EMBL; ALO21480; CAAL6327.1; -
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGREAMS; TIGR01297; CDF; 1.
SEQUENCE 391 AA; 42389 MW; 41F126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Y39E4A.2a protein. Y39E4A.2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               045922;
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                      none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                                                                      108
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                                                                                                     GVLYYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLH--QSGHGHSHGTTN----
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                                          TDAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQ
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VMRDIFFVLMEATPSHYDLSDVKKALSALEGVKGVHDLHLWSIGMDKTAFSVHLALESPN
                                                                                                                                                         HSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVT
                                                                                                                                                                                 HCHYWDENDDDMVARVERGGSTDSASSREDTGRRAEKVLWAVAALSAVFIAAEFVGGFWA
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                                                                                                                                                                                                                                                                                                                                                         sequence of the nematode
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                (JAN-1998)
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                          42389 MW; 41F1260CEA4F6BD6 CRC64;
                                                                                                                                                                                                                             36.5%; Score 702; DB 5;
40.6%; Pred. No. 3.4e-52;
tive 76; Mismatches 102
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01-NOV-1998 (
01-NOV-1998 (
01-JUN-2002 (
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC005310; AAC33498.1; -
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
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NCBI_TaxID=3702;
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Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudiocytyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
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                           ALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIE
                                                                                                                            YFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVE
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AVHELHIWAITVGKVLLACHVNIRPEADADMVLNKVIDYIRREYNISHVTIQIE
                                                                                                    LVAAFGLVVNIIMAVLLGHDHGHSHGHGHGHGHDHHNHSHGVTVTTHHHHHHDHEHGHSHG
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37.9%;
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71; Mismatches
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edons; core eudicots; Rosid
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MEDLINE-21396513; PubMed-11481436;

A PETSANS M.W. Nieman K., Salt D.E.;

Persans M.W. Nieman K., Salt D.E.;

I "functional activity and role of cation-efflux family meml hyperaccumulation in Thlaspi goesingense.";

I Proc. Natl. Acad. Sci. U.S.A. 98:9995-10000(2001).

R EMBL; AY044454; AAK91871.1; -

R EMBL; AY044455; Cation_efflux.

R InterPro; IPR002524; Cation_efflux.

R Pfam, PF01545; Cation_efflux; 1.

R TIGRFAMS; TIGR01297; CDF; 1.

Q SEQUENCE 360 AA; 39555 MW; 612BAFAE8DB2301F CRC64;
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Best Local
                                                                    Zinc transporter ZAT.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                       09ZT63; PRELIMINARY;
09ZT63;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
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 STRAIN=CV. ECOTYPE
MEDLINE=99169295; P
                             SEQUENCE FROM N.A.
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PubMed=10069843;
             C24;
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transport protein MTP1t2
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Pred. No. 1.1e-47;
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eudicots; Rosid
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Q9LXS1;
Q1-OCT-2000
                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/Ge
EMBL; AL353032; CAB68298.1;
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
D'Angelo M., Vezzi A., Modesto D., Pigazzi M.,
D'Angelo M., Vezzi A., Modesto D., Pigazzi M.,
Rudd S., Lemcke K., Mayer K.F.X., Quetier F., !
Rudd S., Lemcke K., Mayer B., Quetier F., !
Rudd S., Lemcke K., Mayer M.F.X., Quetier F., !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Physiol. 119:1047-1055(1999).
EMBL; AF072858; AADI1757.1; -.
InterPro; IPR002524; Catton_efflux.
Pfam; PF01545; Catton_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                 Score 642; DB 10;
Pred. No. 4.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 643.5;
Pred. No. 3.7
Pred. No. 4.70
9; Mismatches
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Q93XE9;
01-DEC-2001 (TrembLrel. 1
01-DEC-2001 (TrembLrel. 1
01-JUN-2002 (TrembLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assuncao A.G.L., da Costa Martins P., de Folter S., Vooij Schat H., Aarts M.G.M.;

"Elevated expression of metal transporter genes in three the metal hyperaccumulator Thlaspi caerulescens.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE275750; AAK69428.1;

InterPro: IPR002524; Catton_efflux.

Pfam; PF01545; Catton_efflux; 1.

TIGRFAMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thlaspi caerulescens.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Thlaspi.
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9; Mismatches
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MEDLLNE=21396513; PubMed=11481436;

MEDLLNE=21396513; PubMed=11481436;

Persans M.W., Nieman K., Salt D.E.;

Persans M.W., Nieman K., Salt D.E.;

"Functional activity and role of cation-efflux family

"Functiona
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Pfam; PF01545; Cation_efflux; 1.
TIGREAMS; TIGR01297; CDE; 1.
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392 AA; 43121
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Pred. No. 1.1e-46;
5; Mismatches 92,
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Zinc transporter.
Fairbairn D.J., Day S., Gomez-Gallego S., Sawbridge T., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF197329; AAL25646.1; -
InterPro; IPR002524; Cation_efflux. Pfam; PF01545; Cation_efflux; 1.
TIGR71297; CDF; 1.
SEQUENCE 421 AA; 46495 MW; A42AA9AEFA2DA46A CRC64;
                                                                                                                                                                                                                                                                        Eucalyptus grandis.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Myrtales; Myrtaceae; Eucalyptus.
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InterPro; IPR002524; Cation_efflux. Pfam; PF01545; Cation_efflux; 1.
TIGRRAMS; TIGR01297; CDF: 1.
TIGRRAMS; TIGR01297; CDF: 1.
SEQUENCE 392 AA; 43080 MW; D6C691017BD9194F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                     CHAQKGPDSHCDPKKG-KAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDF
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                                                                                                                                             CNHQPGFRANSKSKSAQEAKYKIMLAVALCCVFMIIEFLGGYVAGSLAIMTDAAHLASDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFHTVTIQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDSIQSVGVMIGGAIIWIKPEWTIVDLICTLIFSVIVLGTTIRMLRNILEVLMESTPREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHHHHGEDSKGHADQLHGHETDQTEPLLQTCSEAEGDSKLGAKQKQQRNINMQGAYLHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVNIAMALLLGHDHSHGHGHDHGHGHSHGHDDAHEHSDHAHSHEDHGDLHTHGLTIKKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEATPROSYGFFRIEILGALVSIQIIWLLAGILVYEAIERLINGTTEVHGFLMFIIAAFG
  EIDGGTMLITSGCAVAVNIIMGLTLHQS----
                                                ISFVIGLVAIWIGGRPPDERMSFGYKRFEVIGALASILGIWFVTTLLVVVAIERIFSQDF
                                                                                          ASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDY
                                                                                                                                                                                                                                         129;
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                                                                                                                                                                                                                                    76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
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Pred. No. 4.8e-46;
8; Mismatches 91;
                                                                                                                                                                                                                                    Score 605.5; DB 5;
Pred. No. 9.2e-44;
6; Mismatches 102;
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  -GHGHSH--
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C.J.,
Wan
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Best Local
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                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AL138642; CAB71901.1; -.
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
SEQUENCE 334 AA; 37344 MW; B0357A942A052E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choisne N., Robert C., Brottier P., Winc
Artiguenave F., Saurin W., Weissenbach J
Mayer K.F.X., Quetler F., Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; educotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                          TPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSR 340
                                                                       FIHVIGDEMQSMGVLVAAYILYEKPEYKYVDPICTEVESILVLGTTLTILRDVILVLMEG
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                                                                                                                    VLVAAFGLVVNIIMIVVLGHDHGHGHDHGHSHDHGHSYGERAEQLLEKSKEIRNINVQGA 198
                                                                                                                                                SSSDAKKRAASMRKLCFVVVLCLLFMSIEVVCGIKANSLAILADAAHLLTDVGAFAISML
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                                                       YLHVLGDLIQSIGVMIGGGMIWYNPKWKVIDLICTLFFSVIVLGTTIKMLRSILEVLMES
                                                                                                                                                                             SLWASSWEANPROSYGFFRIEILGTLVSIQLIWLLTGILVYEAVTRLVQETNDDVDGFFM
                                                                                                                                                                                                         SLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLI-SGDYEIDGGTM 178
                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                              31.1%;
                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                               Score 599; DB 1
Pred. No. 2e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J., Mewes H.W., Lemcke K.,
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                                                                                                                                                                                                                                                                                                                           Length 334;
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Qy
                                                                        RX MEDLINE-20195005; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., RA George R.A., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Bellew R.M., Basu A., Buck J., Brokstein P., Bothikov S., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Dowles P., Davles P., Davles P., Davles P., Center A., Chardy S., Dahlke C., Davenport L.B., Davles P., Ra Dorkov B.C., Dun D.E., Dohnes M., Dugan-Rocha S., Dunkov B.C., Dun D. Dowles P., Center A., Devis S.M., Roder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M. D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Lasko P., Lei Yt. Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Yt. Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Alexand D., Weitsky A.A., Li J., Lin Y., Moshrefi A., Ra Shue B.C., Stapleton M., Strong R., Sun E., Shen H., Ra Shier E., Yao Q.A., Yang S.Y., Yao Q.A., Yang S.Y., Yao Q.A., Yang G.Y., Yao Q.A., Ya
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                   Query Match
Best Local Similarity
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9V9I1;
01-MAY-2000
                                                                                         EMBL; AE003785; AAF57308.1; --
FlyBase; FBgn0025593; BEST:CK02137.
InterPro; IPR002524; Cation_efflux.
Pfam; PF01595; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
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BEST:CK02137 OR CG11163.
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Conservative
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                   29.4%;
33.5%;
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13,
21,
 66;
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Score 565; DB 5;
Pred. No. 2.5e-40;
6; Mismatches 88
                                                                          5863806608A88857
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Matches 114
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9ZW23;
O9ZW23;
O1-MAY-1999 (TrEMBLrel. 10,
O1-MAY-1999 (TrEMBLrel. 10,
O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ database: InterPro; IPR002524; Cattion_efflux.

Pfam; PF01545; Cattion_efflux; 1.
TIGRPAMS; TIGR01297; CDF; 1.
SEQUENCE 385 AA; 43534 MW; 49A7B564F57FDC2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotylaedons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN=CV. COLUMBIA;
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QRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATK 130
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29.8%;
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Pred. No. 7.
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Q8SQT3;
01-JUN-2002 (
                                                                                                                                                                                                                                                              MEDLINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                     "Genome sequence and gene compaction of the eukaryote parasite Encephalitozon cuniculi.";
Nature 414:450-453(2001).
EMBL: AL590450; CAD26061 1;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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FGFIVSLLSLSWAKKPSNKRMIFGYHRIEIIGSMVSIGLIWAAVGYLVIESFHKYLH-PA
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                                 -GIAVVGFFVNCICIYVLHYDEYQH
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InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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54; Mismatches
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Bentley S.D., Parkhill J.,
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Q9X7Q7;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                       InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMs; TIGR01297; CDF; 1.
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EMBL; AL049587; CAB40701.1;
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Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative efflux protein. SC06751 OR SC5F2A.34C.
                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Redenbach M., Kieser H.M.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1902;
                                                                                                                                                                                                                                        Hopwood D.A.;
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                                                    312 AA;
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e EMBL/GenBank/DDBJ databases.
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Last annotation updat
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    16;
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  Length
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Baquero F., Berche P., Bloecker H., Brandt P., Chakrabortty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Ra Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Ra Lian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Ra Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Coience 294.849-852(2001).

RESEL, ALS91983; CAD00653.1; -.
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                                                                                                                          InterPro; IPR002524; Cation_efflux.

Pfam; PF01545; Cation_efflux; 1.

TIGRRAMs; TIGR01297; CDF; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 303 AA; 33140 MW; BE32A94EA3FE81FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; 1
Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical LMO2575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8Y480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8Y480
                                                                                                                                                                                                      ListiList; LMO02575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes.
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AHNHDHAHGHNHNHAHNANKK-----SLFISFILIATFMVVEVIGGIMTNSLALLSDAGH
                              AQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHFDVEHCTFQLEPSGHAEHEARLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KFHFHTVTIQIEDYSEDMKDCQACQ 368
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                                                                          Similarity
                                                             21.6%;
llarity 30.1%;
Conservative 7
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                                                             Score 414.5; DB 1
Pred. No. 1.3e-27;
2; Mismatches 127
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                                                             Indels
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ISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIG

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                                                                                                          Matches
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Best Local
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                              Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Chatchit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Yoss H., Wehland J., Cossart P.;
                                                                                                                                                                                                    InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMs; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
EMBL; AL596173; CAC97946.1; -.
ListLList; LIN02720; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-CLIP 11262 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeriaceae; Listeria.
NCBI_TaxID=1642;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lin2720.
                                                                                                                                                                      Hypothetical protein; Complete SEQUENCE 303 AA; 33165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q927R8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285
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LLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERL
                                                           AQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVD | : |: | : : | : | : | : | : | : | | | | | | | | |
                                            AHNHDHAHGHNHNHTHNANKK-----SLFISFILIATFMIVEVIGGIMTNSLALLSDAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHTVTIQIE
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                                                                                                                          Similarity
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                       21.3%; Score 410.5; DB 16; 30.4%; Pred. No. 2.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Clostridium group; Bacillales;
                                                                                                          70;
                                                                                                        Pred. No. 2.900; Mismatches
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                                                                                                                                                                      proteome.
AAC6D63CC5473422 CRC64;
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                                                                                                                                      Length
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N [1]
SEQUENCE FROM N.A.

REQUENCE FROM N.A.

REDLINE=92079888; PubMed=1745226;
RA Kiel J.A., Boels J.M., Beldman G., Venema G.;
RT "Molecular cloning and nucleotide sequence of the glycogen branching RT enzyme gene (glgB) from Bacillus stearothermophilus and expression in RT Escherichia coli and Bacillus subtilis.";
RL Mol. Gen. Genet. 230:136-144(1991).

RRI InterPro; IPR002524; Cation_efflux.
DR Pfam; pF01545; Cation_efflux; 1.

TIGRFAMS; TIGR01297; CDF; 1.

TIGRFAMS; TIGR01297; CDF; 1.

"CPONTENCE 316 AA; 35833 MW; 20253115697D7A23 CRC64;
RESULT
Q99X53
ID Q9
AC Q9
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Best Local S
Matches 82
Q99X53;
Q99X53;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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Q1-MAY-2000 (TTEMBLrel. 13, Created)
01-MAY-2000 (TTEMBLrel. 13, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
ORF 2 upstream of GLGB coding region.
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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                                                                                       HLWAVSTDHYSLTAHVFISEHIQPFCVILAINEMLNKKYGIKHTTIQVE
                                                                                                         HIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIE
                                                                                                                            Y-FFDPLISIIIAAIIFTGGAKIIRESYLILMEAVPDQFNLDQIRGDIRQIEGVEDVHDM
                                                                                                                                                                    IVNLILTIILSRS------TKEEENLNIKSALWHFIGDLLSSIGVIISAILIYFTGF
                                                                                                                                                                                                                         PATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAV
                                                                                                                                                                                                                                               QNQSKKTLWITLVLTLFFTIVEIVGGLLSNSLALLSDSAHMASDVLALGLSMIALYLAMR
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                                                                                                                                                YKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSL
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                                                                                                                                                                                                                                                                                      Conservative
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Last sequence update)
Last annotation update)
                    Created)
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                  Bacillaceae; Bacillus NCBI_TaxID=1423;
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NCBI_TaxID=158878,
 SEQUENCE FROM N.A.
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                                                                                                                                                                                     HTVTIQIED
                                                                                                                                                                                                                                                                                                                                                                                                      93;
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"Whole genome sequencing of meticillin-resistant aureus.";
Lancet 357:1225-1240(2001).
EMBL; AP003358; BAB56330.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain Mu50 / ATCC Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillus/Clostridium
YRDO OR CZCD.
Bacillus subtilis.
Bacteria; Firmicutes;
                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Cation transport protein YRDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 36235 MW; AA5C27E49D5F3157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002524; Cation_efflux. Pfam; PF01545; Cation_efflux; 1. TIGREPAMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.aureus (strain Mu50), an MEDLINE=21311952; PubMed=11418146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMGVLVAAYILYFKPEYKYVDDICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAV
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                                                                                                                                                                                                PRELIMINARY;
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       Bacillus/Clostridium
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No. 2.1
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    group; Bacillales;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bouriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borliss R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Galizron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Alota R., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sechuseks A., Serror S.J., Serror R., Scoffone F.,
RA Viatra A., Wambutt R., Wedler E., Wedler R., Wedler E., Yognoni A.,
RA Viatra A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Ratkeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Voshida K., Vanamoto H., Yamane K., Yasumoto K., Yata K.,
Ra Voshida K., Valados S., Vandenoto H., Yanane K.,
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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[3]
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   HIWALTVAQPVLSVHIAIAQN---TDAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKD
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                                                            YKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSL
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Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative in Brucella melitensis.";
proc. Natl. Acad. Sci. U.S.A. 99:443-448(2)
EMBL; AE009580; AAL52619.1; -
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRPAMS; TIGR01297; CDF; 1.
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Q8YFT2;
01-MAR-2002
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;

STRAIN=16M / ATCC 23456 / BIOTYPE 1;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Muje Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., R. Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., R. Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M. Jablonski L., Larsen P.H., Hagius S., O'Callaghan D., Letess Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letess
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NCBI_TaxID=29459;
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Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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                                    Q99SB4 PRELIMINARY; PRT;
Q99SB4-3001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
CZIB protein (Cation-efflux System me
CZIB OR SAV2146 OR SA1948.
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Submitted
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"Characterization of a gene cluster for glycogen biosynthesis heterotetrameric ADP-glucose pyrophosphorylase from Bacillus stearothermophilus.";
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Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacill
Geobacillus.
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Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
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01-JUL-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
             Staphylococcus aureus
                          Staphylococcus aureus (strain Mu50 /
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MEDLINE=95031021;
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BL; D87026; BAA19587.1; -
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317 AA;
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27.5%;
(strain N315).
Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
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Last sequence up
Last annotation
                                                              Last sequence up
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Pred. No. 9.1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 110;
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Lancet 357:1225-1240(2001).
EMBL; AP003364; BAB58308.1; -.
EMBL; AP003136; BAB43232.1; -.
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGREAMS; TIGR01297; CDF; 1.
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Q9ZNF5;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2002
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  Kuroda M., Hayashi H., Ohta "Chromosome-determined zinc aureus strain 912.";
Microbiol. Immunol. 0:0-0(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.aureus (strain Mu50), and MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                Staphylococcus aureus Bacteria; Firmicutes; Staphylococcus.
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                                                                                              STRAIN=912;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=1280;
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3; Mismatches
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Pred. No. 1
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SEQUENCE
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InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
SEQUENCE 325 AA; 36130 MW; 1C5D
                                                                                                                                                        InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRPANS; TIGR01297; CDF; 1.
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                                                                                                                                                                                            Gene 188:91-94(1997).
EMBL; U62055; AAB53029.1; -.
                                                                                                                                                                                                                     Sturr M.G., Ablooglu A.J., Krulwich T.A.; "A Bacillus subtilis locus encoding sever transport of cations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  P71023
                                                                                                                                                                                                                                                         MEDLINE=97254454; PubMed=9099864;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
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ALVSVLSIWVVTGYLYYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGH
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                                   YMITEAIGGFLTNSLALLSDAGHMLSDSISLMVALTAFTLAEKKANHNKTFGYKRFETLA
                                                           FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILG
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97; Conserv
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                                                                                                                                   32404 MW;
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                                                                                             20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%; Score 390; DB 2; 1
29.3%; Pred. No. 1.9e-25;
Live 73; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium group;
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21,
                                                                                   81;
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Last sequence update)
Last annotation update)
                                                                                 Score 388.5; I
Pred. No. 2.2e<sup>-</sup>
81; Mismatches
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InterPro; IPR002395; Kininogen.
Pfam; PF01545; Cation_efflux; 1.
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RC STRAIN-ARCC 15692 / PAO1;

RX MEDLINE-20437337; Pubmed=10984043;

RX MEDLINE-20437337; Pubmed=10984043;

RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Stover R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

RA Garber R.L., Goltry L., Tolger K.R., Kas A., Larbig K., Lim R.M.,

RA Frody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.";

RI Nature 406:959-964(2000).

REMBL; AE004477; AAG03786.1; -.

REMBL; AE004477; AAG03786.1; -.

REMBL; AE004477; AAG03786.1; -.

DR Ffam; PF01545; Cation_efflux.

Pfam; PF01545; Cation_efflux.

Complete Strokenser.
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Matches 88
                    085143;
01-NOV-1998
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2 (TrEMBLrel. 21, Las
ation efflux system p
                  3 (TrEMBLrel.
3 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                               PRELIMINARY;
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Last annotation updat
em protein.
                                       Created)
Last sequence update)
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Pred. No. 5.9e
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                       Last annotation
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.9e-24;
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                       update)
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Query Match
Best Local S
Matches 92
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01-MAY-2000 (TrEMBLrel. 13, C

01-MAY-2000 (TrEMBLrel. 13, I

01-JUN-2002 (TrEMBLrel. 21, I

CG17723 protein (LD22804P).
         MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Brandon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tacheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                          CG17723
                                                                                                                                                                                                                                                                                                                              Q9VZR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance to zinc and cobalt ions J. Bacteriol 180:4024-4029(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiong A., Jayaswal R.K.;
"Molecular characterization of a chromosomal determinant conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98361887; PubMed=9696746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-RN450;
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                                                                                                                                                                                                                                                                                                                                                                                                       284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSVGAITAA-ILIWAFGWTIADPIASILVSVIILKSAWGTTKSSINILMEGTPSDVDIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-EVQSKEMLIISIIGLIVNIVVAFFRFKGG---
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Pro; IPR002524; Cation_efflux.
PF01545; Cation_efflux; 1

AMS; TIGR01297; CDF; 1

NCE 326 AA; 36233 MW; 4731
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FHTVTIQIEDYSEDMKDCQACQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 28.2
92; Conservative
 Agbayani
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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 An H.-J.,
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                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.2e
71; Mismatches
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                                                                                                                                                                                               Diptera;
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1.2e-23;
135;
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                                                                                                                                                                                                            Hexapoda;
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                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DHTLTMKECELLLENIEHDLL
                                                                                                                                                                                                Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTSHNLNMRGAFLHVIGDLL
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   c.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AE003477; AAR47754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0035432; CG17723. InterPro; IPR002524; Cation_efflux.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          124
                                         242 VLILHSVWPLLRESALILLQTVPTHIQVDAIQKRLLEKVDGVLAVHEFHVWQLAGDRIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
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                                                                                                                                                                                                                                                   VNIIMGLTL---HQSGHGHSHG---TTN------
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                                                                                                                                                                                                                                                                                                             WSKN-TFGWARAEVLGALVNAVFLVALCFSITIEACKRFIEEEPIHEPELLVIVGALGLL
                                                                                                                                                                                                                                                                                                                                                      ATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVA
SVHIAIAQNTDAQAVLKTASSRLQGKFH---FHTVTIQIEDYSEDMKDCQACQGPS
                                                                    ILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLL-SVEGVEALHSLHIWALTVAQPVL:|:|: | :| |:| |:| |: ::
                                                                                                                              SSHGHSHDPGQMMMRGAFLHVLSDALGSIIVVISAVVVW-KTEWKYRYYMDPALSIVLV
                                                                                                                                                     -----SVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYK---YVDPICTFVFS
                                                                                                                                                                                                                     VNVI-GLCLLYEHGGHHGHSHGGGLTRNHSRLTELANMDEGEDEQNDFAYEKQKEKAPVK
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AMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 366; 28.9%; Pred. No. 3.
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Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ge R.,
C.J.,
Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
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Q98H85;
Q06808 PRELIMINARY; PRT; 429 AA.
Q06808;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Qxidative stress resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 7:331-38(2000).
EMBL; AP003000; BaB49981.1; -.
InterPro: IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRENAS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 365 AA; 38979 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome structure of the nitrogen-fixing Mesorhizobium loti.";
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Best Local S
Matches 97
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SGD; S0004856; ZRC1.

InterPro; IPR002524; Cation_efflux.

Pfam; PF01545; Cation_efflux; 1.

TIGRFAMS; TIGR01297; CDF; 1.

SEQUENCE 429 AA; 47075 MW; B41C7957D99980E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93332654; pubMed=8338639;
Inoue Y., Kobayashi S., Yoshikawa K., Tran L., Kimura A.;
"Lipid hydroperoxide-resistance gene in Saccharomyces cerevisiae:
utilization as a selectable marker gene for yeast transformation.";
Biotechnol. Appl. Biochem. 17:305-310(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inoue Y., Kobayashi S., Kimura A.;
J. Ferment. Bioeng. 75:327-331(1993).
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                                                                                                                                                                                                                               SNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAIS 183
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                          FH---FHTVTIQIE----DYSEDMK 362
                                                         SADQIQREILAVPGVIAVHDFHVWNLTESIYIASIHVQI----DCAPDKFMSSAKLIRKI 358
                                                                                                                                                                                                                                                                                                                 TKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAV 188
FHQHGIHSATVQPEFVSGDVNEDIR
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25.2%; Pred. No. 1.8e-22;
tive 80; Mismatches 108;
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C2CD_ALCED
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ZNT1_YEAST
COT1_YEAST
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ZNT1_BCOSI
YM43_YEAST
YEAB_BACST
YM43_YEAST
YM49_METJA
YQR5_CAEEL
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Q62941;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Zinc transporter 2 (ZnT-2).
SLC30A2 OR ZNT2.
         DOMAIN
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 TRANSMEM
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                                                                                                               Pfam; PF01545; Cation_efflux; TIGRFAMs; TIGR01297; CDF; 1.
                                                                                                                                          EMBL; U50927;
                                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                               facilitating vesicular sequestration.";
EMBO J. 15:1784-1791(1996).
                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Kidney; MEDLINE-96203098; PubMed-8617223;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZNT2_RAT
                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                Palmiter R.D., Cole T.B., Findley S.D.; "ZnT-2, a mammalian protein that confers resistance
Transport;

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SWMEM 57

SWMEM 87

SWMEM 124

SWMEM 124

SWMEM 145

SWMEM 160

SWMEM 160

SWMEM 181

SWMEM 208

SWMEM 208
                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
LOCALIZED IN THE MEMBRANE OF ENDOSOMAL VESICLES
TISSUE SPECIFICITY: INTESTINE, KIDNEY, SEMINAL V
                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                      FUNCTION: INVOLVED
                                                                                                                                                                                                                                                                                               VESICLES.
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IPR002524; Cation_efflux.
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                                                                                          Transmembrane; Multigene family; Repeat CYTOPLASMIC (POTENTIAL).
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YAF3_YEAST
NQ68_PARDE
CYB_BUNFA
CYB_GULGU
CYB_HIPNI
CYB_DASAL
CYB_DASAC
FEM2_RAT
AD15_MOUSE
NKC1_HUMAN
YLD1_CAEEL
CYB_PELSU
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VACUOLAR (POTENTIAL).
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15-JUN-2002 (Rel. 4
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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STRAIN=129; TISSUE=Brain;
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              SWISS-PROT entry is copyright. It is produced through a collaboration
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Rodentia;
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80.1%;
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        of Bioinformatics
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                             Zinc transporter 3 (ZnT-3).
SLC30A3 OR ZNT3.
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15-JUN-2002 (Rel. 41, Last annotation
                                                                    Q99726;
30-MAY-2000
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         Homo sapiens (Human)
Eukaryota; Metazoa;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                          361
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                                                                                                                                                                                                                                                                                                                                                                                                      EKQHLLDARPAIRSYTG-----SLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1345280; Slc30a3
                                                                                                                                          GFSSCTLQVEQYQPEMAQCLRCQEPS
                                                                                                                                                    HFHTVTIQIEDYSEDMKDCQACQGPS
                                                                                                                                                                                                                                 GDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILTDVILVLMEGTPKGV
                                                                                                                                                                                EFEPVRDTLLSVPGVRATHDLHLWALTLTYHVASAHLAIDSTADPEAVLAEASSRLYSRF
                                                                                                                                                                                          DFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKF
                                                                                                                                                                                                                       GDLLQSFGVLAASILIYFKPQYKVADPISTFLFSICALGSTAPTLRDVLLVLMEGAPRSV
                                                                                                                                                                                                                                                             LLTASIAVCANLLMAFVLHQTGAPHSHGSTGAEYAPLEEGHGYPMSLGNTSVRAAFVHVL
                                                                                                                                                                                                                                                                         LITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQ----EE------NSVRAAFIHVI
                                                                                                                                                                                                                                                                                                     FSLWLSTRPATRTMTFGWHRSETLGALASVVSLWIVTGILLYLAFLRLLHSDYHIEAGAM
                                                                                                                                                                                                                                                                                                              PQSGLSPERVQARRQLYAACAVCFIFMAGEVVGGYLAHSLAIMTDAAHLLADIGSMLASL
                                                                                                                                                                                                                                                                                                                                                     PDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISL
                                                                                                                                                                                                                                                                                                                                                                                    ETTRLVSARD--RSSAGGGLRLKSLFTEPSE--PLP-----EEPKLEGMAFHHCHKDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF01545; Cation_efflux; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U76008; AAB39733.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002524; Cation_efflux.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR01297; CDF;
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96
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41824 MW;
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                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                   52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1006.5;
Pred. No. 1.6e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
POTENTIAL.
VACUOLAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3CCDD0A37074EF41 CRC64;
                                                                                                                                          386
                                                                                                                                                            371
                                                 on update)
                                                                                         388
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                                                                                                                                                                                                                                                                                                                                                                                                                                     .6e-67
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          SAHLAIDSTADPEAVLAEASSRLYSRFGFSSCTLQVEQYQPEMAQCLRCQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01545; Cation_efflux; 1.
TIGRFAMS; TIGR01297; CDF; 1.
Zinc_transport; Transport; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U76010; AAB39732.1; -Genew; HGNC:11014; SLC30A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palmiter R.D., Cole T.B., Quaife C.J., Findley S.D.;
"2NT-5, a putative transporter of zinc into synaptic vesicles.";
Proc. Natl. Acad. Sci. U.S.A. 93:14934-14939(1996).
-!- FUNCTION: INVOLVED IN ACCUMULATION OF ZINC IN SYNAPTIC VESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Temporal cortex;
MEDLINE=97121493; PubMed=8962159;
Palmiter R.D., Cole T.B., Quaife
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   32 PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
LOCALIZED IN THE MEMBRANE OF SYNAPTIC VESICLES (PROBABLE)
SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                         GYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSI
                                                  SILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVL
                                                                                                                                                                            WVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQ
                                                                                                                                                                                                                            GYLAHSLAIMTDAAHLLADVGSMMGSLFSLWLSTRPATRTMTFGWHRSETLGALASVVSL
                                                                                                                                                                                                                                                                                       PLPE---ESKPVEMPF---HHCHRDPLPPPGLTPERLHARRQLYAACAVCFVFMAGEVVG
SVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQGP
                                                                                               YAPLEEGPEQPLPLGNTSVRAAFVHVLGDLLQSFGVLAASILIYFKPQYKAADPISTFLF
                                                                                                              ----EENP------SVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVF
                                                                                                                                                             WMVTGILLYLAFVRLLHSDYHIEGGAMLLTASIAVCANLLMAFVLHQAGPPHSHGSRGAE
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        388
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                                                                                                                                                                                                                                                                                                                                                                     50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Multigene family. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      Score 972.5;
Pred. No. 5.2e
50; Mismatches
                                 TPRNVGFEPVRDTLLSVPGVRATHELHLWALTLTYHVA
                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
74B8E24F17CF4740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC POTENTIAL.
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                    Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNAPTIC VESICLES
 370
                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                             258
                                                                                                                                                             213
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RESULT 4
ZNT4_HUM2
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                                                                                         Query Match
Best Local
                                            Matches
                                                                                      DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                   MIM;
                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc transporter 4 (ZnT-4).
SLC30A4 OR ZNT4.
                                                                                                                          DOMAIN
                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                          Pfam; PF0154
                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                        EMBL; AF025409;
                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fetal brain;
MEDLINE=98016412; PubMed=9354792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             014863;
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                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                  TIGREAMS; TIGR01297; CDF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel gene involved
                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                      Zinc
                                                                                                                                                                                                                                                                                                       InterPro;
 56
                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPARTMENT.

SUBCELLULAR LOCATION: Integral membrane protein.

LOCALIZED IN ENDOSOMAL VESICLE MEMBRANE (PROBABLE).

LOCALIZED IN ENDOSOMAL VESICLE MEMBRANE (PROBABLE).

DOMAIN: CONTAINS A HISTIDINE-RICH REGION WHICH IS A LIGAND ZINC AND AN ASPARTIC ACID-RICH REGION WHICH IS A POTENTIAL FOR ZINC (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FANTRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 17:292-297(1997).
FUNCTION: PROBABLY INVOLVED IN ZINC TRANSPORT OUT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASM, MAY BE BY SEQUESTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                     EAKEKQHLLDARPAIRSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDS 61
                                                                                                                                                                                                                                                                     transport;
                                                                                                                                                                                                                                                                                                                   602095;
EAPERP-VNGAHPTLQADDDSLLDQD---LPLTNSQLSLK-----VDSCDNCSKQRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L., Gitschier
                                                                                                                                                                                                                                                                                                                              HGNC:11015;
                                                       Similarity
                                                                                                                                                                                                                                                                                                      IPR002524; Cation_efflux
                                                                                     241
429
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217
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275
                                            Conservative
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                                                                                                                                                                                                                                                                                             Cation_
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                                                                                        47496 MW;
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                                            ; 88
                                                                                                                                                                                                                                                                     Transmembrane; Multigene family.
                                                     Score 722.5; DB 1
Pred. No. 1.9e-46;
                                                                                                  ASP-RICH (ACIDIC).
HIS-RICH.
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                    POTENTIAL
                                                                                                                                                VACUOLAR
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                                                                                        538992DFF8768739 CRC64;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                               milk mouse.";
Nat. Genet. 17:292-297(1997).
-i- FUNCTION: PROBABLY INVOLVED IN ZINC
CYTOPLASM, MAY BE BY SEQUESTRATION 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc transporter 4 (ZnT-4) (Lethal milk protein).
SLC30A4 OR ZNT4 OR LM.
                                                                       This
                                                                                                                                                                                                                                                            COMPARTMENT.

COMPARTMENT.

CONTION: Integral membrane protein LOCALIZED IN ENDOSOMAL VESICLE MEMBRANE (PROBAB-

TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHLY EX-
BRAIN AND IN MAMMARY EPITHELIAL CELL LINES.

DOMAIN: CONTAINS A HISTIDINE-RICH REGION WHICH ZINC AND AN ASPARTIC ACID-RICH REGION WHICH IS
                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98016412; PubMed=9354792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
STRAIN-C57BL/6, at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                035149;
                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang L., Gitschier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                         A novel gene involved in
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                                                                                                                                          FOR ZINC (BY SIMILARITY).

DISBASE: LETHAL MILK (LM) MICE ARE DEFECTIVE IN ZINC TRANSPORT INTO BREAST MILK, DUE TO A PREMATURE TRANSLATION TERMINATION CODON AT POSITION 297. ONLY HOMOZYGOUS MUTANT ADULTS DEVELOP DERMATITIS, SKIN LESIONS, AND HAIR LOSS DUE TO A SYSTEMIC ZINC DEFICIENCY. HOMEVER NEONATAL MICE (OF ANY GENOTYPE) SUCKLED ON HOMOZYGOUS MUTANT FEMALE ALSO DEVELOP SYMPTOMS CHARACTERISTIC OF NUTRITIONAL ZINC DEFICIENCY, INCLUDING DERMATITIS, ALOPECIA AND STUNTED
                                                                                                   GROWTH.
SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMYRCTIQLQSYRQEVDRTCANCQSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLQGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGCAVAVNIIMGLTLHQSGHGHSHGTT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                           zinc
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OTENTIAL
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RESULT ZNT4_R/ID ZNT4_R/ID ZNT4 CO.
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Best Local S
Matches 148
         SULT 6
TT4_RAT
TT4_RAT
STANDARD; PRT; 430 AA.
055174;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
2inc transporter 4 (ZnT-4) (Dri 27 protein).
SLC30A4 OR ZNT4.
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DOMAIN
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                                                                                                                                                                                                                                   IHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGT:| :|| :|| :|| :|| :|| :|| ::::::||
                                                                                                                                                                                                                                                                                                                                                                                                   EAPERP-VNGAHPALQADDDSLLDQD---LPLTNSQLSL------KMDPCD
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                                                                                                                                                       RLQGKFHFHTVTIQIEDYSED-MKDCQACQGPS 371
                                                                                                                                                                                                                                                                  VMLITAAVGVAVNVIMGFLLNQSGHHHSHAHSHSLPSNSPSMVSSGHNHGQDSLAVRAAF
                                                                                                                                                                                                                                                                              TMLITSGCAVAVNIIMGLTLHQSGHGHSHGTT------
                                                                                                                                                                                                                                                                                                            TLLALWLSSKSPTRRFTFGFHRLEVLSAMISVMLVYVLMGFLLYEAVQRTIHMNYEINGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1345282;
                                                                                                                                  LLLNTFGMYKCTIQLQSYRQEVIRTCANCQSSS 429
                                                                                                                                                                             PSHLNVDYIKESLMKIEDVYSVEDLNIWSLTSGKSTAIVHMQLIPGSSSKWEEVQSKAKH
                                                                                                                                                                                                  PKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASS
                                                                                                                                                                                                                         VHALGDLVQSVGVLIAAYIIRFKPEYKIADPICTYIFSLLVAFTTFRIIWDTVVIILEGV
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AF004097; AAB82411.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF004099; AAB82413.1; -. AF003747; AAB82593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF004100;
 norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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179
200
217
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297
312
333
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47791 MW;
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143
164
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37.7%;
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CYTOPLASMIC
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Pred. No. 5
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CYTOPLASMIC
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E2311FA6265D15C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                 update)
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.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SÜBÜNIT: MEDIATES HETERODIMERIC INTERACTIONS WITH AT LEAST ONE SPECIFIC PARTMER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane (probable). IN THE LOCALIZED IN ENDOSOMAL VESICLE MEMBRANE (PROBABLE). IN THE POLARIZED ENTEROCYTES, IT IS MAINLY LOCALIZED IN THE BASAL CYTOPLASMIC REGION.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHLY EXPRESSED IN BRAIN AND TESTES. ALSO EXPRESSED IN SMALL INTESTINE, MEDUILA, LUNG, KIDNEY, STOMACH, AND COLON. EXPRESSED AT LOWER LEVEL IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murgia C., Vespignani I., Cerase J., Nobili F., Perozzi G.;
"Cloning, expression, and vesicular localization of zinc tran"?
"7/2n74 in intestinal tissue and cells.";
Am. J. Physiol. 277:G1231-G1239(1999).
-i- FUNCTION: PROBABLY INVOLVED IN ZINC TRANSPORT OUT OF THE CYTOPLASM, MAY BE BY SEQUESTRATION INTO AN INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Wistar; TISSUE=Brain; MEDLINE=20068535; PubMed=10600821;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y16774; CAA76372.1;
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: DEVELOPMENTALY REGULATED IN THE INTESTINE. INDUCTION: NO CHANGE IN RESPONSE TO ZINC DEPRIVATION.

DOMAIN: CONTAINS A HISTIDINE-RICH REGION WHICH IS A LIGAND FOR ZINC AND AN ASPARTIC ACID-RICH REGION WHICH IS A POTENTIAL LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
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DOMAIN DOMAIN DOMAIN SEQUENCE TRANSMEM Pfam; PF01545; Cation_efflux; TIGRFAMs; TIGR01297; CDF; 1. DOMAIN TRANSMEM DOMAIN TRANSMEM TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN Zinc transport; InterPro, IPR002524; Cation_efflux. DOMAIN 430 AA; Transport; 134 143 1164 1178 1199 1216 2375 2375 2375 2375 2375 2375 2375 47702 MW; Transmembrane; Multigene family. CYTOPLASMIC (POTENTIAL). CYTOPLASMIC POTENTIAL.
VACUOLAR (POTENTIAL. Score 711; Ub 1, No. 1.3e-45; CYTOPLASMIC (POTENTIAL)
ASP-RICH (ACIDIC).
HIS-RICH. POTENTIAL.
VACUOLAR (POTENTIAL). CYTOPLASMIC (POTENTIAL) POTENTIAL. POTENTIAL. F34CED3FA4FF05FB CRC64 (POTENTIAL). (POTENTIAL). (POTENTIAL)

20

HCDP-----KKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLI 116

NCSKRRELLKQRKVKTRLTIAAVLYLLFMIGELVGGYMANSLAIMTDALHMLTDLSAIIL

В Q

Matches Query Match Best Local

150;

Conservative

85;

pred. No. 1.36
5; Mismatches

116;

42;

Gaps

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KMDPCD

96 6

Length 430 Indels

Similarity

37.0%;

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EAKEKQHLLDARPAIRSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDS

EAPERP-VNGAHPALQADDDSLLDQE---LPLTNSQLSL---

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                                                                                                                                                      or send an
                                                                                                                                                                entities
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                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                McCielland M., Sanderson K.E., Spieth J., Clifton S.W., La
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mil
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534940; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium
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                                                                                              TIGRFAMs;
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                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restrest by non-profit institutions as long as its content is filed and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-sities.requires.alicense.agreement)
                                                                                                                                                                                                                                                                         FUNCTION: Involved in zinc efflux across the cytoplasmic membrane, thus reducing zinc accumulation in the cytoplasm and rendering bacteria more resistant to zinc. It may contribute to zinc homeostasis at low concentrations of zinc (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein (Potential).

SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY OF
                                                                                                                                                                                                                                                                TRANSPORTERS (CDF, TC
                                                                                                                                                                                                                                                                                                                                                                                                    E., Sun H., Florea L. rston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLIALWISSKSPTRFTFGFHRLEVISAMISVMLVYVLMGFILYEAMQRTIHMNYEINGD
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                                                                                                SG?????; zitB
; TIGR01297; C
  Zinc
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48
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M., Du F., Hou S., Layman D.,
                                                                                 Complete
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Best Local
                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of a enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
-i- FUNCTION: Involved in zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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ZITB OR STY0799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                        FUNCTION: Involved in zinc efflux across the cytoplasmic menthus reducing zinc accumulation in the cytoplasm and renderbacteria more resistant to zinc. It may contribute to zinc homeostasis at low concentrations of zinc (By similarity). SUBCELLULAR LOCATION: Integral membrane protein (Potential) SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAM. TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                            SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., Barrell B.G.;
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Pred. No. 3e-25;
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P75757;
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01-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
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MEDLINE-97061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita M., Kanai K., Kashimoto K.,
Ikemoto K., Indda T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
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TRANSMEM
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
Mau B., Shao Y.;
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MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
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STRAIN-K12 / MG1655;
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                                                                                              complete genome sequence of nce 277:1453-1474(1997).
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Pred. No. 5e-25;
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                                                                                                       Escherichia coli K-12.";
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                                                                                                                                       Burland V.,
yhew G.F.,
                                                                                                                              D.J
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LLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTI

MCREIPEVRNVHHVHVW-MVGEKPVMTLHVQVIPPHDHDALLDQIQHYLMDHYQIEHATI

VLVAAYILYFKPEYKYVDPICTFVFSILVLGTTTLTILRDVILVLMEGTPKGVDFTAV-RD

-TGWTPADPILSILVSLLVLRSAWRLLKDSVNELLEGAPVSLDIAELKRR

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DGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMG

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LLFALLAVQFSRRPPTIRHTFGWLRLTTLAAFVNAIALVVITILIVWEAIERFRT-PRPV

Best Loc Matches Query Match

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Similarity

22.4%;

Conservative

69;

Score 431; DB Pred. No. 5.1e 69; Mismatches

5.1e-25; nes 121; DB 1;

Indels

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Gaps

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SEQUENCE

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DOMAIN

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Grass G., Fan B., Rosen B.P., Franke S., Nies D.H., Rensing C.;

"21tB (YbgR), a member of the cation diffusion facilitator family, is
an additional zinc transporter in Escherichia coli.";
J. Bacteriol. 183:4664-4667(2001).

-i. FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
thus reducing zinc accumulation in the cytoplasm and rendering
bacteria more resistant to zinc. It may contribute to zinc
homeostasis at low concentrations of zinc, whereas zntA is
required for growth at more toxic concentrations.

-i. SUBCELULAR LOCATION: Integral membrane protein (Potential).

-i. INDUCTION: By zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yano M., Horluch ...
"A 718-kb DNA sequence of the E corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                  the
                                                                                              Transport;
                                                                                                                          Pfam; PF01545; Cation_efflux; 1. TIGRFAMs; TIGR01297; CDF; 1.
                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       entities requires a license agreement
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                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                       InterPro;
                                                                                                                                                                   EcoGene; EG13662; zitB.
                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content is ified and this statement is not removed. Usage by and for the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: Appears to be selective for zinc, not conferring resistance to cobalt nor cadmium.
SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY
                                                                                                                                                                                                                                                                                                                            TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                              D90714; BAA35414.1;
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Horiuchi T
                          ; Zinc transport; 1
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                                                                                                                                                      IPR002524; Cation_efflux.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc transporter zitB.
ZITB OR Z0922 OR ECS0780.
Escherichia coli 0157:H7.
                                                                                                                   DOMAIN
CONFLICT
                                                                                                                                                               TRANSMEM TRANSMEM
                                                                                                                                                                                                             TRANSMEM TRANSMEM
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EC057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                         Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
[2]
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MEDLINE-21156231; PubMed-11258796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Involved in zinc efflux across the cytoplasmic membrane, thus reducing zinc accumulation in the cytoplasm and rendering bacteria more resistant to zinc. It may contribute to zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homeostasis at low concentrations of zinc (By similarity). SUBCELLULAR LOCATION: Integral membrane protesin (Potential). SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. 8:11-22(2001).
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AP002553;
                        Similarity
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158
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                                                                                           311 AA;
  Conservative
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                                                                                           MW;
69;
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HIS-RICH.
MA -> MAHS
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Tanaka M., Tobe T.,
                                           Length 311;
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RESULT 11
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P13512;
01-JAN-1990
01-NOV-1997
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            "Two-component regulatory system involved in transcriptional of heavy-metal homoeostasis in Alcaligenes eutrophus.";
Mol. Microbiol. 23:493-503(1997).
-!- FUNCTION: NECESSARY FOR ACTIVATION OF THE CZC DETERMINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35
15-JUN-2002 (Rel. 41
Cobalt-zinc-cadmium
                                                                                                                                                                                              -!- INDUCTION: BY ZINC.
-!- SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97197194; PubMed=9044283; Wen der Lelie D., Schwuchow T., Schaeyens W., Mergeay M., Nies D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nies D.H., Nies A., Chu L., Silver'S.; "Expression and nucleotide sequence of a plasmid-determined cation efflux system from Alcaligenes eutrophus."; proc. Natl. Acad. Sci. U.S.A. 86:7351-7355(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenes eutrophus (Ralstonia Plasmid pMOL30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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TRANSMEM 47
TRANSMEM 47
TRANSMEM 82 1
                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P94178;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                       "Cloning and sequence analysis of czc CT14.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Kunito T., Kusano T.,
Matsumoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-96219090;
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     EMBL; D67044; BAA11062.1;
                                                                                                                                                                                                                                                                                                                                            Biosci. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alcaligenes sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cation efflux system protein czcD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=512;
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                                                                                                                                                                                                                                                                                                        SCI. Blotechnol. Blochem. 60:699-704(1996).
FUNCTION: NECESSARY FOR ACTIVATION OF THE CZC DETERMINANT
                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY
                                                                                                                                                                                                                                            TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHCDPKKGKAQRQLYVASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRF-TGWAWVDSAIAVLIGLWVLPRTWILLKSSLNVLLEGVPDDVDLAEVEKQILATPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYI
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PF01545; Cation_efflux; 1.
AMs; TIGR01297; CDF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Strain CT14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8829543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; potenti a potenti 67 potenti 102 potenti 135 potenti 135 potenti 172 potenti 172 potenti 172 potenti 174 potenti 194 potent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 388;
Pred. No. 7
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2977C1B4AEE9600F CRC64;
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ZITB_YERPE
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                                 Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; The Genome sequence of versinia pestis, the causative agent of plague."; Nature 413:S23-527(2001).

The FUNCTION: Involved in zinc efflux across the cytoplasmic membrane, thus reducing zinc accumulation in the cytoplasm and rendering bacteria more resistant to zinc. It may contribute to zinc homeostasis at low concentrations of zinc (By similarity).

TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                     STRAIN-CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungal
                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq)
15-JUN-2002 (Rel. 41, Last anno
Zinc transporter zitB.
ZITB OR YPO1129.
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                Yersinia pestis
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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C., Mungall K.L.,
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P20107;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
ZIRC1 OR YMR243C OR YM9408, 05C.
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  SEQUENCE FROM N.A. STRAIN-S288c / AB972; Gentles S., Bowman S. Submitted (MAR-1995)
                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                       Kamizono A., Nishizawa M., Teranishi Y., Murata "Identification of a gene conferring resistance ions in the yeast Saccharomyces cerevisiae."; Mol. Gen. Genet. 219:161-167(1989).
                                                                                                                                                                                       MEDLINE=90136503; PubMed=2693940;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-DKD-5D-H;
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EMBL/GenBank/DDBJ da
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Pred. No. 2.8
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                                                                                 MQSMGVLVAAYILYFKPEYK---YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGV
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FHQHGIHSATVQPEFVSGDVNEDIR
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I (IN REF. 1).
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                                                                                                                                                                                                                                                                                                           .2e-19
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F ZINC OR CADMIUM
D BE INVOLVED IN
F ZINC OR CADMIUM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
Cobalt uptake protein COT1.
COT1 OR YOR316C OR O6131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92375034; PubMed=1508175;
Conklin D.S., McMaster J.A., Culbertson M.R.,
"COT1, a gene involved in cobalt accumulation
                                                                                                                                                                                 InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
TIGRRAMS; TIGR01297; CDF; 1.
Transport; Cobalt; Mitochondrion; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
      CONFLICT
                  CONFLICT
                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 12:1021-1031(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweizer M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c / FY1679;
MEDLINE=97051589; PubMed=8896266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROBABLY RESPONSIBLE FOR THE UPTAKE OF COBALT IONS. IT APPEARS TO ACT IN A DOSAGE-DEPENDENT MANUER TO COUNTERACT THE APPEARS TO ACT IN A DOSAGE-DEPENDENT MANUER TO COUNTERACT THE APPEARS TO ACT IN A DOSAGE-DEPENDENT MANUER TO COUNTERACT THE APPEARS OF COBALT IONS ON CELLS. IT MAY PARTICIPATE IN THE REGULATION OF COBALT LEVELS UNDER NORMAL PHYSIOLOGICAL CONDITIONS AND MAY BE IMPORTANT IN THE SUPPLY OF METAL THAT IS REQUIRED FOR METALLOENZYME OR COFACTOR SYNTHESIS. IT REDUCES THE TOXICITY OF COBALT AND RHODIUM IONS. OTHER COMPONENTS RESPONSIBLY TOXICITY OF COBALT AND RHODIUM IONS. OTHER COMPONENTS RESPONSIBLITE FOR COBALT TRANSPORT EXIST.

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE, ANOTHER POSSIBILITE EXISTS THAT IT IS ASSOCIATED WITH ANOTHER UNIDENTIFIED MEMBRANE THAT HAS BEEN ENRICHED IN THE MITOCHONDRIAL MEMBRANE FRACTIONS. SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR FAMILY OF THE MASSOCIATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                                                                                           ; M88252; AAA74884.1; -.; x90565; CAA62171.1; -.; Z75224; CAA99636.1; -. S31302; S31302.
                                                                                                                                                                                                                                            S0005843;
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XV reveals regions
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HIS-RICH; COULD I
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HI -> RV (IN REF. :
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                                                                                                                                                                                    Transmembrane.
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in Saccharomyces
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Best Local :
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Q62720;
30-MAY-2000;
30-MAY-2000;
15-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
                                                              "Regulation of the zinc transporter ZnT-1 by dietary Proc. Natl. Acad. Sci. U.S.A. 95.4841-4846(1998).
-!- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT O.:- SUBUNIT: MULTIMER (PROBABLE).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE).
                                                                                                                                                                                                                       Palmiter R.D., Findley S.D.; "Cloning and functional characterization of transporter that confers resistance to zinc
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  Zinc transporter 1 (ZnT-1). SLC30A1 OR ZNT1.
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                                                                                                                                             McMahon R.J., Cousins R.J.;
                                                                                                                                                        TISSUE=Intestine;
MEDLINE=98226729; PubMed=9560190;
                                                                                                                                                                                                              EMBO
                                                                                                                                                                                                                                                                          TISSUE=Kidney;
                                                                                                                                                                                                                                                            MEDLINE=95188868; PubMed=7882967;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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  BASOLATERAL SURFACE OF THE ENTEROCYTES. THE PROTEIN IS DET TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN IS DET DUDDENUM AND JEJUNUM BUT NOT IN ILEUM AND COLON. INDUCTION: SLIGHTLY BY ZINC IN THE INTESTINE, BUT NOT THE SIMILARITY: BELONGS TO THE CATION DIFFUSION FACILITATOR
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439 AA;
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(Rel. 41, Last annotation
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48154 MW;
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Pred. No. 6.
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                                            RESULT 17
ZNT1_MOUSE
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Best Local Sim
Matches 105;
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CARBOHYD
ZNT1_MOUSE
Q60738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TIGRFAMs; TIGR01297; CDF; 1.
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                                                                                                                                           420 FASVGSKSSVVPCELACR
                                                                                                                                                                                          356
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                                                                                                                                                                                                                                                                                                                                   304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPORTERS (CDF, TC 2.A.4). SLC30A SUBFAMILY.
                                                                                                                                                                                     DYSEDMKD----CQ-ACQ 368
                                                                                                                                                                                                                                   GVEEVHELHVWQLAGSRIIATAHIKCEDPASYMQVAKT----IKDVFHNHGIHATTIQPE
                                                                                                                                                                                                                                                                             GVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH----FHTVTIQIE
                                                                                                                                                                                                                                                                                                                              MHEAGPCWVLYLDPTLCIIMVCILLYTTYPLLKESALILLQTVPKQIDIKHLVKELRDVE
                                                                                                                                                                                                                                                                                                                                                                     EYK-----YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQEETNTLVANTSNSNGLKADQAEPEKLRSDDPVDVQVNGNLIQESDSLESEDNRAGQLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt MRGVFLHVLGDALGSVIVVVNALVFYFSWKGCTEDDFCVNPCFPDPCKSSVELMNSTQAP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRAAFIHVIGDFMQSMGVLVAAYILYFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLVNVLGLCLFHHHSGEGQGAGHGHSHGHGHGHLAKGARKAGRAGGEAGAPPGRAPDQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRNRGRLLCMLLLTFMFMVLEVVVSRVTASLAMLSDSFHMLSDVLALVVALVAERFARRT
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                      STANDARD;
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24.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 335; DB 1;
Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
6 X 2 AA APPROXIMATE REPEATS
N-LINKED (GLCNAC. . .) (POTEN;
9F9770017C2455FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                      503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
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Best Local S
Matches 103
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SEQUENCE
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Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Palmiter R.D., Findley S.D.;

Extractional Confers resistance to zinc.";

EMBO J. 14:639-649(1995).

PALMIT OF KNOCKOUT EARLY IN GESTATION SUGGESTS A ROLE OF THE PROTEIN IN FETAL ZINC ACQUISITION SUBGESTS A ROLE OF THE PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.

PROTEIN IN FETAL ZINC ACQUISITION EXEMPTION.

PROTEIN MULTIMER (PROBABLE).

PALMITER OF THE PLASMA MEMBRANE (PROBABLE).

PALMITER OF THE PLASMA MEMBRANE (PROBABLE).

PALMITER SPECIFICITY: WIDELY EXPRESSED.

PALMITER SPECIFICITY: BELONGS TO THE CATTON DIFFUSION FACILITATOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Zinc transporter 1 (ZnT-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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124
                             187
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LLVNVLGLCLFHHHSGEGQGAGHGHSHGHGHGHLAKGARKAGRAGVEAGAPPGRAPDQEE
                           AVNIIMGLTL -- HQS ----- GHGHSHG --
                                                                           -ATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAV 186
                                                                                                               GRNRGRLLCMLLLTFMFMVLEVVVSRVTASLAMLSDSFHMLSDVLALVVALVAERFARRT 64
                                                                                                                                          GKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1345281;
                                                       HATQKNTFGWIRAEVMGALVNAIFLTGLCFAILLEAVERFIE-PHEMQQPLVVLSVGVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01545; Cation_efflux; 1. AMS; TIGR01297; CDF; 1.
                                                                                                                                                                       103;
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002524; Cation_efflux.
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                                                                                                                                                                       Conservative
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Rođentia;
                                                                                                                                                                                    17.3%;
23.7%;
                                                                                                                                                                                                                              Œ;
                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Multigene family; Repeat.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                    Score 333; DB
Pred. No. 1.5e
72; Mismatches
                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).

6 X 2 AA APPROXIMATE REPEATS OF H-G
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                            7C4FF93FC13CDA22 CRC64;
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                                                                                                                                                                                    .5e-17;
                                                                                                                                                                                                  DB 1;
                                                                                                                                                                       121;
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                                                                                                                                                                                                Length 503;
                                                                                                                                                                       Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
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 183
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RESULT 18
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ID 3C63_S
AC P74068
AC P74068
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DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Yamada M., Yasuda 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
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01-NOV-1997
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AMS; TIGR01297; CDF; 1.
                                 Similarity
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                                                                                                                 10 3C
44 66
78 9
113 13
161 1F
310 AA;
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1 protein s111263.
   Conservative
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                                                                                                                              30 F
64 F
98 F
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33324 MW;
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   65;
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POTENTIAL.
POTENTIAL.
                                 Score 173;
Pred. No. 6.
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POTENTIAL.
822C5946CBEC7122 CRC64;
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RESULT 19
YGLIB_BACST
ID YGLIB_B
AC 930540
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DT 01-APR
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DE Hypoth
OS Bactl1
OC Bacter
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                                                                                                                                TRANSMEM NON_TER
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"Molecular cloning and nucleotide sequence of the glycogen branching enzyme gene (glgB) from Bacillus stearothermophilus and expression in Escherichia coli and Bacillus subtilis.";

Mol. Gen. Genet. 230:136-144(1991).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical protein in GLGB 5'region (Frag
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacill
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01-APR-1993 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                              Hypothetical
TRANSMEM
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                                                                                                               SEQUENCE
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    PF01545; Cation_efflux; 1.
hetical protein; Transmembrane
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108 /
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55 75
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                                                                                                             108
12046 MW;
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75
                                                              8.0%; Score 153; DB 1; 29.2%; Pred. No. 6.1e-05;
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                                               35;
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                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geobacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
(Fragment).
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                                                28;
                                                                              Length 108
                                               Indels
                                                0
                                               Gaps
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Вb

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QNQSKKTLWITLVLTLFFTIVEIVGGLLSNSLALLSDSAHMASDVLALGLSMIALYLAMR

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Matches 70
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MEDLINE-97109536; PubMed-8951816;
MEDLINE-97109536; PubMed-8951816;
Ferson A.E., Wray L.V., Fisher S.H.;
Ferson A.E., Wray L.V., Fisher S.H.;
"Expression of the Bacillus subtilis gabp gene is regulated
"Expression of the Bacillus subtilis gabp and amino acid availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borriss R., Porwollik S., Schroeter R.;
"The 52 degrees-55 degrees segment of the Bacillus subtilis chromosome: a region devoted to purine uptake and metabolism, and containing the genes cotA, gabP and guaA and the pur gene cluster within a 34960 bp nucleotide sequence.";
Microbiology 142:3027-3031(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P46348; 005001;
01-NOV-1995 (Rel. 32,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACSU
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EMBL; U31756; AAC44640.1; -.
EMBL; Z99107; CAB12451.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  independently in response to nitrogen and amino acid Mol. Microbiol. 22:693-701(1996).
-I- SUBCELLULAR LOCATION: Integral membrane protein
-I- SIMILARITY: BELONGS TO THE UPF0018 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97124186; PubMed=8969499;
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                                                                    KKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSS
KPPDEDHPYGHFRAETIASLIASFIMMVVGLQVLFSAGESIFSAKQETPDMIAAWTAAGG
                         RPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEI-DGGTMLITSGC
                                                     KKGESGALVSIAAYLVLSAI--KLIIGYLFHSEALTADGLNNTTDIIASVAVLIGLRISQ
                                                                                                                            Similarity
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                                                                                                                                                                             1 protein; 35 35 35 82 102 113 133 133 134 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                          Score 143; DB 1;
Pred. No. 0.00098;
                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                Mismatches
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AHNPLLVLSTEQIRKNAGVRITWVGLGVNVGIAIGKFFGGIVFHSQALFADAIHAISDMV 202

--KKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFA 112

-SLNLHSHTHSHGHTHSHA

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RESULT 21
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
Hypothetical 56.2
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 56.2 kDa protein in SIP18-SPT21
YMR177W OR YM8010.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 249808; CAA89910.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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EAKEKQHLLDARPAIRSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S0004789; YMR177W
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Ms; TIGR01297; CDF; 1.
                                                                                                                Similarity
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                                                                                                                                                                                                                      510 AA;
                                                                                                                                                                                                                                                                                   1 protein;
165 185
194 214
241 261
286 306
333 353
                                                                               Conservative
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214
261
306
353
376
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                                                                                                            6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane
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POTENTIAL.
                                                                                                                Pred.
                                                                                                                                                 Score 132.5;
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                                                                                                                                                 Length
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p32159;
01-CCT-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 27, Last sequence upda
16-CCT-2001 (Rel. 40, Last annotation up
Hypothetical protein yiip.
YIIP OR B3915 OR E5459 OR ECS4840.
                                                                                                                                                                                                                                                                                                                       Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli oli7:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A. Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plunkett G. III, Burland V.D., Daniels D.I Plunkett G. III, Burland V.D., Daniels D.I "Analysis of the Escherichia coli genome. region from 87.2 to 89.2 minutes."; Nucleic Acids Res. 21:3391-3398(1993).
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          PIR; S40858; S40858.
EcoGene; EG11873; yilp.
InterPro; IPR002524; Cation_efflux.
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / RIMD UDUYYDZ;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
MEDLINE=93347969; PubMed=8346018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21074935; PubMed-11206551;
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                                                            AE000466;
AE005622;
AP002567;
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                                                                                                            L19201; AAB03047.1; -.
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Cation_efflux;
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AAG59108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli 0157:H7.";
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MEDLINE-96337999; PubMed-8680897;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrangean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                      jannaschii.",
Science 273:1058-1073(1996).
SCIENCE LIULAR LOCATION: Integ
-i- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                        Submitted
                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                    Hypothetical F19C6.5.
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                                                                      ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. Then by non-profit institutions as long a lifted and this statement is not removed. Ities requires a license agreement (See I send an email to license@isb-sib.ch).
                                                                                                                                                       nitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                           SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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МJ0449;
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01545; Cation_efflux; 1.
3; TIGR01297; CDF; 1.
3; TIGR01297; CDF; 1.
POTENTIAL.
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
1 28.6 kDa protein F19C6.5 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VGKKLNSQVLIADAYHHRSDALSSVVVLVG--LLLQKFGIYYGDAIAGIIVAL
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                                                     CAA88049.1;
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                                                                                                                                                                                                                                      Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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4F9128C4222365FE CRC64;
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RESULT 25

KE4L_CAEEL

ID KE4L_CAEEL

ID CAEC

AC Q9XTQ7

DT 16-OCT

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DT 16-OCT

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CO CRABDGI

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                                                                                                                                                                                                                                                                                     EMBL; Z99942; CAB17070.1;
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                                                                                                                                                                                                                                                                                                                                                              modified
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    -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
    -!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                  InterPro;
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; IPR002395; Kininogen
                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                         KININOGEN
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CARBOHYD
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                                                                                                                                                                                                                                                                                             Perry E.A., Carr S.M., Bartlett S.E., Davidson W.S.;

"A phylogenetic perspective on the evolution of reproductive behav
in pagophilic seals of the Northwest Atlantic as indicated by
mitochondrial DNA sequences.";

J. Mammal. 76:22-31(1995).

--- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS.

--- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q35468; Q35466;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on the true se
J. Mol. Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arnason U., Bodin K., Gullberg A., Ledje C., Mouchaty S.; "A molecular view of pinniped relationships with particular on the true seals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-95230701; PubMed-7714914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTCYB OR COB OR CYTB.
Phoca hispida (Ringed seal) (Pusa hispida).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYB_PHOHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-134 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9718;
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                                                                                                                                                                                              BOUND TO THE PROTEIN.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE:
CYTOCHROME C1 AND THE RIESKE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TALGALSGCVISLFSADADALADAAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LA--IGASFIAGTTVGIV-TMITVLVHEVPH-----EIGDFAILIQSGYSKKKAMLIQLV
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20.8%;
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Pred. No. 1.3;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
17D7E854F4E1DAAF CRC64;
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                              (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
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                                                      for commercial
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RESULT 27
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Best Local S
Matches 69
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Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
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SEQUENCE
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                                             Synechocystis by strong 64% to 92% of the genome. ; region from map positions 64% to 92% of the genome. ; DNA Res. 2:153-156(1995).

-!- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+)
-!- CATALYTIC ACTIVITY: NADH + plastoquinone protein
                                                                                                                                                                                                                                    NADH-plastoquinone oxidoreductase chain 5 (EC NDHF OR SLR0844.
 This
                                                                               Sugilira M., Tabata S.;
Sugilira M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the I Mb
Synechocystis sp. strain PCC6803. I. Sequence features in the I Mb
                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00032; cytochrome_b_C; Pfam; PF00033; cytochrome_b_N;
                                        -!- SUBCELLULAR LOCATION: Integral memba
                                                                                                                                              Kaneko T., Tanaka A., Sato S.,
                                                                                                                                                                                                                                                                                                                     NU5C_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ICLLFMIGEVVGGYLA-----HSLAVMTDAAHLLTDF-------ASM-LISLF-
                          OF CHLOROPLASTS OR MITOCHONDRIA
SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICLILQI--LTGLELAMHYTSDTTTAFSSVTHICRDVNYGWIIRYLHANGASMFFICLYM 96
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L39205; AAC28748.1;
P00157; 1BE3.
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97
182
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379
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(Rel. 35, Last sequence up)
(Rel. 40, Last annotation
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IRON 2 (HEME B566 A)
IRON 2 (HEME B562 A)
IRON 1 (HEME B566 A)
IRON 1 (HEME B566 A)
905FF04B79EE7E12 (
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Pred. No. 1.3;
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Mismatches
                                                                                                                                              Kotani H., Sazuka
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 It is
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produced through a collaboration
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                                                               plastoquinol
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RESULT 28
CYB_ORNAN
ID CYB_O
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DT 01-NO
DT 30-MA
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OS OFFICE
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TRANSMEM
                                                      Cytochrome B.
MTCYB OR COB OR CYTB.
Ornithorhynchus anatinus
                                                                                     Q36461;
01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
30-MAY-2000 (Rel. 39,
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NCBI_TaxID=9258;
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus
                                            Mitochondrion.
                                                                                                                                  CYB_ORNAN
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1_N.
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(Ornithorhynchus anatinus).";
J. Mol. Evol. 42:153-159(1996).
-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX) OF THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X83427; CAA58454.1; ...
InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME;
PROSITE; PS00193; CYTOCHROME_B_QO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE-Heart, and MEDLINE-97077300;
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SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1
CYTOCHROME C1 AND THE RIESKE PROTEIN.
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYB_DROYA
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InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b(1.
Pfam; PF00033; cytochrome_b(1.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC ACIDS RES. 12:3747-3762(1984).
-:- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C RECOMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHERESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clary D.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-2317.6 Ivory Coast; MEDLINE-86089137; PubMed-3001325.
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"Sequence and arrangement of the genes for cytochrome b, URI
"RE4, URE5, URE6 and five tRNAs in Drosophila mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84221393; PubMed=6328435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUPLED TO ATP SYNTHESIS.

(COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH BOUND TO THE PROTEIN.

SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME C1 AND THE RIESKE PROTEIN.

SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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                                                                                                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                  PS00192; CYTOCHROME_B_HEME; PS00193; CYTOCHROME_B_QO; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene organization, and
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(Rel.
(Rel.
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07, Last sequence up
39, Last annotation
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Neoptera; Endopterygota; Diptera; Braci
oidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                              Mitochondrion;
                                                                                                43137
                        5.1%;
18.7%;
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R
                      Score 99;
Pred. No.
                                                                                           IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
; 868491DE01B031AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Drosophila yakuba: genetic code.";
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                                                                                                                                                                                                                                         Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                               DB
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                                               Length 378
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                                                                                                                                                                                                                                              Transmembrane;
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WHICH IS
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65; Conserv

Conservative

54;

Mismatches

Indels 118;

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16;

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CYB_CYSCR
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                                                                                              "A phylogenetic perspective on the evolution of reproductive behavior in pagophilic seals of the Northwest Atlantic as indicated by mitochondrial DNA sequences.";

J. Mammal. 76:22-31(1995).

-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.

-i- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARP NOT COMPLEY OF THE PROTETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-95230701; PubMed=777149

Arnason U., Bodin K., Gullberg

"A molecular view of pinniped
on the true seals.";
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 51-130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalogy, Kansas (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Intra- and interfamilial systematic relationships indicated by mitochondrial DNA sequences."; (In) Dizon A.E., Chivers S.J., Perrin W.F. (eds); Molecular genetics of marine mammals, pp.277-290, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr S.M., Perry E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-134 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cystophora cristata.
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MTCYB OR COB OR CYTB.
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                  BOUND TO THE PROTEIN.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1
CYTOCHROME C1 AND THE RIESKE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOCHROME B FAN
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K., Gullberg A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g A., Ledje C., relationships
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Pinnipedia;
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                                                                         CYTOCHROME
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RESULT 32
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Best Local S
Matches 69
                                                                                                                                                                                                                                      CYB_PHATA
Q35673;
15-JUL-1998
15-JUL-1998
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
CONFLICT
                                                                                                                                                                   Cytochrome B.
MTCYB OR COB OR CYTB
Phascogale tapoatafa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
  MEDLINE=93096825; PubMed=1361058;
Krajewski C., Driskell A.C., Bave
                                                                                                             Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prosite; ps00192; CYTOCHROME_B_HEME;
prosite; ps00193; CYTOCHROME_B_QO; 1
mitochondrion; Electron transport; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00032; cytochrome_b_C;
Pfam; PF00033; cytochrome_b_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X82294; CAA57737.1;
EMBL; L19124; AAA74098.1;
EMBL; L39209; AAC28750.1;
HSSP; P00157; IBE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                            SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=9293;
                                                                                                                                                     Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                        , Metazoa; C
Metatheria;
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36,
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182
196
130
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                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                Created)
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IRON 2 (HEME B566 A)
IRON 2 (HEME B562 A)
IRON 1 (HEME B566 A)
IRON 1 (HEME B566 A)
G -> S (IN REF. 2).
W; 6CAC4C6044EED898 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98.5; D
Pred. No. 2.6;
12; Mismatches
                                                                                                                                                                       wambenger).
    Baverstock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VLGTTLTILRDVILVLME-GTPKGVDFTAVRDLLLS
                                                                                                                                 Craniata;
                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HEME B566 AXIAL LIGAND).
(HEME B562 AXIAL LIGAND).
(HEME B566 AXIAL LIGAND).
(IN REF 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HEME B562 AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                               381
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There are no rescription as its content to the content to
                                                                                                             Dasyuridae;
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    P.R.,
                                                                                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                               ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
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                                                                                                             Phascogale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 117;
                                                                                                                                   Euteleostomi;
    M.J.;
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RESULT ZNT4_BO ID ZN AC Q9 DT 30 DT 15 DT 15 DE Z1
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Best Local
                ZNT4_BOVIN
Q9TTF3;
30-MAY-2000 (
30-MAY-2000 (
15-JUN-2002 (
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 among
                                                                                               BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. R. Soc. Lond., B. Biol. Sci. 250:19-27(1992).

-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
-COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M99459; AAB40404.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Phylogenetic relationships of the thylacine (Mammalia: Thylacinidae)
among dasyuroid marsupials: evidence from cytochrome b DNA
sequences.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                              158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 ICLLFMIGEVVGGYLA-----HSLAVMTDAAHLLTDF------ASM-LISLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOUND TO THE PROTEIN.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE:
CYTOCHROME C1 AND THE RIESKE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUPLED TO ATP SYNTHESIS
                                                                                                                                                       PVSQTL----
                                                                                                                                                                                      AVRDLLLSVEGVEALHSLHIWALTV------AQPVLSVHIAIAQ
                                                                                                                                                                                                                                                   ---YFKPEYKYVDPICTFVFSIL----VLGTTLTILRDVILVLM-----EGTPKGVDFT
                                                                                                                                                                                                                                                                                  GINPDSDKIP-----FHPYYTIKDALGAVLLLLVLLLLALFSPDSLGDPDNFSPANPLN
Nr-2000 (Rel. 39, Created)
Nr-2000 (Rel. 39, Last sequence update)
Nr-2002 (Rel. 41, Last annotation update)
transporter 4 (ZnT-4) (Fragment).
                                                                                                                                                                                                                     TPPHIKPEWYFL----FAYAILRSIPNKLGGVLALLASILILLIIPLLHTANQRSMMFR
                                                                                                                                                                                                                                                                                                                 GTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYIL-------
                                                                                                                                                                                                                                                                                                                                                                            L-----VYLAVERLISGDYEIDGGTM-----LITSGCAVAVNIIMGLTLHQSGHGHSH 205
                                                                                                                                                                                                                                                                                                                                                                                                             HVGLGIYYGSYLYKETWNIGVILLITVMATAFVGYVLPWGQMSFWGAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SLWMSSRPATKTMNFG---------WQRAEILGALVSVLSIWVVTGV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICLMIQI -- LTGFFLAMHYTSDTLTAFTSVAHICRDVNYGWLLRNLHANGASMFFMCLFL
                                                                                                                                                                                                                                                                                                                                              LSAIPYIGTTLAEWIWGGFAVDKATLTRFFAFHFILPFIIVALAIVHLLFLHETGSNNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR000179; Cyt_b_b6.
PF00032; cytochrome_b_C;
PF00033; cytochrome_b_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00192; CYTOCHROME_B_HEME; PS00193; CYTOCHROME_B_QO; 1
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97
182
196
381 AA;
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                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
97
182
196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Mismatches
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IRON
IRON
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Pred. No. 3
                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (HEME B562 AXIAL LIGAND).
2 (HEME B566 AXIAL LIGAND).
2 (HEME B562 AXIAL LIGAND).
1 (HEME B566 AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 133;
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Best Local S
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                               P18275;
01-NOV-1990
01-NOV-1990
15-JUN-2002
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SEQUENCE
protein.";
Gene 87:37-43(1990)
                                                                                                                                                      Arginine/ornithine antiporter. ARCD OR PA5170.
                                                                                                                                                                                                                                    PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF103904; AAF16866.1; -. InterPro; IPR002524; Cation_efflux. Pfam; PF01545; Cation_efflux; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=20078377; PubMed=10612253;
Tammen I., Warren W.C., Raadsma H.W.;
"Physical and linkage mapping of the bovine zinc transporter 4 (ZNT4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                     aeruginosa
                            "The arc operon for
                                                                                                                                                                                                                                                                                                                                                                                                               Zinc transport; Transport; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene to chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                         NCBI_TaxID=287;
                                                                                                                        Pseudomonas
                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                         ARCD_PSEAE
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                                                                                                                                                                                                                                                                             201 HGHSHG-----TT-----NQQEENPSVRAAFIHVIGDFMQSMGVL 235
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                       contains
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                                                                                                                                                                            (Rel. 16, Last sequence update) (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                          Conservative
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44.7%;
                                                                                                                                                                                                                                                                                                                                                                      5159 MW;
                     anaerobic arginine catabolism in Pseudomonas an additional gene, arcD, encoding a membran
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                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                 gamma
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                                                                                                                                                                                                                                                                                                                                    Score 97; DB 1; Length 50; Pred. No. 0.37;
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                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                 subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                         482
                                                                                                                                                                            update)
                                                      Villeval D.,
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                       a membrane
                                                      Mercenier
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004841; Permease.
InterPro; IPR004754; R/O_antiport.
Pfam; PF00324; aa_permeases; 1.
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                                                                                                                                                                                                                                                               TRANSMEM
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Transport; Antiport; Amino-acid transport;
Inner membrane; Complete proteome.
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SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES AN ELECTRONEUTRAL AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ARGININE DEIMINASE PATHWAY.
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                        PIFGKGDTVAAIVCASVLLWALHFLYLRGIKEAAFINTVTTVAKVVPLFLFILICLFAFK 178
                                                PKKGKAQRQLYVASAICLLFMIGEVV--GGYLAHSLAVMTDAAHLLTDFASMLISLFS--
                                                                                                                                                                                                                                                                                                                                                                                                  AE004930; AAG08555.1;
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                                                                                       Similarity
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LWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEI 173
                                                                          Conservative
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C7FC1A7323FB0607 CRC64;
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                                                                                                 1;
                                                                                                                                                                                                                                                                                                             Transmembrane;
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RA Bettinelli A., Ballabio A., Casari G.;
RY Molecular cloning, expression pattern, and chromosomal localization
RY Molecular cloning, expression pattern, and chromosomal localization
RY of the human Na-Ci thiazide-sensitive cotransporter (SLC12A3).";
RY Genomics 35:486-493(1996).
RY OF THE TOWNSTION SELECTRICALLY SILENT TRANSPORTER SYSTEM WHICH IS A
REDIATOR OF SODIUM AND CHLORIDE REABSORPTION.
CHARACTER SOTIUM SELECTROLIVE REABSORPTION.
CHARACTER SOTIUM AND CHLORIDE REABSORPTION.
CHARACTER SOTIUM AND CHLORIDE REABSORPTION.
CHARACTER SOTIUM SECURIANT IN KIDNEY.
CHARACTER SPECIFICITY: PREDOMINANT IN KIDNEY.
CHARACTERIZED BY DIVERSE
CHARACTERIZED B
                                  EMBL; U44128; AAC5
EMBL; X91220; CAA6
Genew; HGNC:10912;
                                                                                                                                                                                                                                                                                                                                                                                This
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MEDLINE=97001149; PubMed=8812482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cotransporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simon D.B., Nelson-Williams C., Bia M.J., Molina A.M., Vaara I., Iwata F., Cushner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS MEDLINE=96122035; PubMed=8528245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiazide-sensitive SLC12A3 OR TSC.
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01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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CAA62613.1;
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                                         SLC12A3
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Primates;
                                                                                                                                                                                                           license agreement
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on update)
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H.M., Koc
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                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                      Usage
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Koolen
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M., Gainza
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*nza F.J.,
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Best Local S
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CONFLICT
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CARBOHYD
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DOMAIN
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InterPro; IPR004842; KCl_cotransport.
InterPro; IPR002948; McL_transporter
PRINTS; PR01230; NACLTRNSPORT.
                                               SEQUENCE
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         57
263800;
                    42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Disease mutat.

1 135 CYTOPLASMIC (POTENTIAL).
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766
807
1021
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                           5.0%;
                                               113138
                          .5%;
                     51;
                                            | T-> P (IN GS).
| FTId=VAR_007125.
| R-> Q (IN GS).
| FTId=VAR_007126.
| AG-> VV (IN REF. 2).
| E-> D (IN REF. 2).
| V-> GARPSVSGAL (IN REF. 1).
| V-> GARPSVSGAL (IN REF. 1).
                    Score 96.5; DI pred. No. 11; Si; Mismatches
                                               Ψ.
                                                                                                                                                                                                               /FTId=VAR_007113.

P -> L (IN GS).
/FTId=VAR_007114.

C -> R (IN GS).
/FTId=VAR_007115.

D -> N (IN GS).
                                                                                                 A -> T (IN GS).
/FTId=VAR_007123.
G -> R (IN GS).
/FTId=VAR_007124.
                                                                                                                                                                                      /FTId-VAR_
MISSING (I
                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> W (IN GS).
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R -> H (IN
                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL) POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                     R -> L (IN GS).
/FTId=VAR_007122
A -> T (IN GS).
                                                                                                                                   /FTId=VAR_007121
R -> L (IN GS).
                                                                                                                                                             /FTId-VAR_007119.
                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                         V (IN GS)
                                                                                                                                               NI) H
                                                                                                                                                                                                    (IN
                                                                                                                                                            (IN GS)
                                                                                                                                                                               (IN GS).
AR_007118.
                                                                                                                                                                                            N GS).
_007117.
                                                                                                                                                      _007120
                                                                                                                                               GS)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                  DΒ
                                1,
                    59;
                                 Length 1021;
                    Indels
                    63;
                    Gaps
                    80
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RESULT 36
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Q9571; Q34733;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                             PROSITE;
                                                                         EMBL; X99256; CAA67640.1; -.
EMBL; L02772; AAA31789.1; -.
InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; Cytochrome_b_C;
Pfam; PF00033; Cytochrome_b_N;
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
 Heme.
METAL
                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           noninvasively from hair. Mol. Phylogenet. Evol. 1 -i- FUNCTION: COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnason U., Gullberg A., Xu X
"A complete mitochondrial DNA
Hylobates lar, and comparison
all hominoid genera.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome B. MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A phylogenetic study of the gibbons (Hylobates) using
noninvasively from hair.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94115700; PubMed=1342936; Garza J.C., Woodruff D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Ester;
                             Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 48-130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hereditas 124:185-189(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hylobates lar (Common gibbon)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 QCLVLTGPPNFRPALVDFVGTFTRNLSLMICGHVL
                                                                                                                                                                                                                                                                                           Phylogenet. Evol. 1:202-210(1992).

FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIT THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.

COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.

SYNTLARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEEN-----
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                                            00032; cytochrome_b_C; 1.
00033; cytochrome_b_N; 1.
ps00192; cytochrome_b_HEME;
ps00193; cytochrome_b_QO; 1
                             transport;
 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVRAAFIHVIGDFMQSMGVLVAAYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                             Mitochondrion; Respiratory chain; Transmembrane;
 83
IRON 1 (HEME B562 AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Eucatarrhini; Hylobatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ule of the white-handed gibbon, individual mitochondrial genes
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                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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ne; Hylobates.
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METAL
                                                                                                                                                 "Complete genome sequence of a multiple drug resistant enterica serovar Typhi CT18.";
Nature 413.848-852(2001).
                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain of Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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                                             SUBCELLULAR LOCATION:
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lesser extent nickel and copper. Involved
oxygen (By similarity).
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                                           VEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGK
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ID MNTH-
AC 09RPF
DT 16-OC
DT 15-JU
DE Manga
GN MNTH-
OS Salnc
OC Bacte
OC Salnc
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16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
15-JUN-2002 (Rel. 41, Last
                                                            Manganese transport MNTH OR STM2408.
                                                                                                                                   MNTH_SALTY
                                                                                                                                                SALTY
NCBI_TaxID=602; [1]
                       Salmonella.
                                   Bacteria; Proteobacteria;
                                                Salmonella typhimurium
                                                                                                                                    STANDARD;
                                                                       protein
                                                                                                           Created)
                                    gamma
                                                                                    sequence up
annotation
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                                     subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kehres D.G., Zaharik M.L., Finlay B.B., Maguire M.E.; "The NRAMP proteins of Salmonella typhimurium and Escherichia coli are selective manganese transporters involved in the response to reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                146
120 FKLILGVSLLQGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELFFSQPDM 179
                                                          63
                                                                                                                                               60 DSHCDPKKGKAQRQLYVA-SAICLLFMIGEVVGGYLAHSLAVMTDAAHLL-----TDFA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: H(+)-STIMULATED, HIGHLY SELECTIVE, MANGANESE UPTAKE SYSTEM. CAN ALSO TRANSPORT CADMIUM, COBALT, IRON, ZINC AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESSER EXTENT NICKEL AND COPPER. INVOLVED IN RESPONSE TO REACTIVE
                                                          AMLIQILSAKLGIATGKNLAEQIRDHYPRP---VVWFYWVQAEIIAMATDLAEFIGAAIG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiol. 36:1085-1100(2000).
                    -----VSVLSIWVVTGVLVYLAVERLISGDYEID---GGTMLITSGCAV-------
                                                                                         SMLISLESLWMS-----
                                                                                                                   DNRVENSSGRAARKLRLALMGPAFIAAIGYIDPGNFATNIQAGASFGYQLLWVVVWANLM
                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               Symport;
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                                                                                                                                                                                                                                      44400 MW;
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                                                                                                                                                                                          Score 96;
Pred. No.
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                                                                                       ----SRPATKTMNFGWQRAEI------LGAL-- 145
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386	177 TMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSV	pb Qy
326	LAMAÑAÑS K.	מַט
17	17 SLFSLWMSSRPATKIMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDG	2 10
116 278	69 KAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLT-DFASMLI	ДУ
aps 9	ery Match 5.0%; Score 96; DB 1; Length 605; st Local Similarity 20.7%; Pred. No. 6.6; tches 52; Conservative 37; Mismatches 102; Indels 60; G	Qи Ве ма
	TRANSMEM 546 566 POTENTIAL. SEQUENCE 605 AA; 67460 MW; 299A89B0E4FCDBC8 CRC64;	SQ
	TRANSMEM 400 420 POTENTIAL. TRANSMEM 423 443 POTENTIAL.	F F T
	TRANSMEM 310 330 POTENTIAL. TRANSMEM 364 384 POTENTIAL.	FT
	TRÂNISMEM 226 246 POTENTIAL. TRÂNISMEM 255 275 POTENTIAL. TRANISMEM 288 308 POTENTIAL.	F F F
	DR EMBL; 271654; CAA96319.1; R SGD; S0005322; YRR039C. W Hypothetical protein: Transmembrane.	DR DR
1	or send an email to license@isb-sib.ch).	දු දු
.ch/announce/	entities requires a license agreement (See http://www.isb-sib.ch/	88
no way	use by non-profit institutions as long as its content is in	38
station -	between the Swiss Institute of Bioinformatics and the EMBL out: the European Bioinformatics Institute. There are no restriction	88
aboration	This SWISS-PROT entry is copyright. It is produced through a coll	86
	Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.	목당
	SEQUENCE FROM N.A. Pohl T.M.:	R.P.
	932;	RN
	Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Carobaromycota; Carobaromycotacaea, Carobaromyce	888
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	STANDARD;	ID AC
	ULT 39	RES
	349LVMSQVLLSFGIALALVPLLIFTSNATLMGE 379	Дb
	IAIAQNTDAQAVLKTASSRLQG	γQ
348	300 LSSTVVGTLAGQVVMQGFVRFHIPLWVRRTITMLPSFIVILMGLDPTRI	рь
296	GTP	Qy
299	240 AIAMTIAGEVNLAMMATAAAAFHESGHTGIADLDQAYLTLEPLLSHAAATVEGLSLVAAG	В
257	220 AFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFV	Qy
239		Db
219	187AVNIIMGLTLHQSGHGHSHGTTNQQEENPSV-RA	Qy

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Wolecular characterization of ferredoxin-NADP+ oxidoreductase in cyanobacteria: cloning and sequence of the peth gene of Synechococcus sp. PCC 7002 and studies on the gene product.";

Blochemistry 31:3092-3102(1992).

-I- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.

-I- SUBCELULAR LOCATION: Integral membrane protein.

-I- SUBCELULAR LOCATION: OF THE NADH-UBIQUINOL OXIDOREDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26,
01-JUL-1993 (Rel. 26,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schluchter W.M., Zhao J., Bryant D.A.; "Isolation and characterization of the ndhF gene of Synechococcus strain PCC 7002 and initial characterization of an interposon mutant.";
                                                            TRANSMEM
                                                                                                                                      Oxidoreductase; TRANSMEM 7
                                                                                                                                                             PRINTS;
                                                                                                                                                                        Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1_N;
                                                                                                                                                                                                                        PIR; A40588; A40588.
InterPro; IPR003916; NADHub_oxred5.
                                                                                                                                                                                                                                                EMBL; M99378; AAA27311.1; -
EMBL; M86234; -; NOT_ANNOTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20 FROM N.A.
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InterPro; IPR001516; Oxidored_q1_N.
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                                                                                                                                                           F00662; oxidored_q1_N;
PR01434; NADHDHGNASE5.
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35, Last annotation update)
oxidoreductase chain 5 (EC
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                                                                                                                              -----LWMSSRPATKTMN--FGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDY
                                                                                                                                                         IVTTVALLVMI--YTDGYMAHDPGYVRFYAYLSIFSSSMLGLVFSPNLVQVYIFWELVGM
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                                                                            LMD----LVSTGQISSLLAIVFAVLVFLG-PVAKSAQFPLHVWLPDAMEGPTPISALIHA
                                                                                              EIDGGTMLITSG-----CAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHV
                                      -----ATMVAAGVFLVARMYPVFEPIPEAMNVIAWTGATTAFLGATIALTQNDIKKG
                                                        IGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKG
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ED60ACF947239BC5 CRC64;
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Pred. No. 7.
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Search completed: March 18, 2003, 15:41:03 Job time : 19 secs

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Title:
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:/cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*
:/cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
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0 US-010-12-542-158

US-10-012-542-33

0 US-09-738-897-3

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US-10-121-049-28

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US-10-175-746-28

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Sequence 22, Appl
Sequence 47, Appl
Sequence 10, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 158, App
Sequence 332, App
Sequence 28, Appli
Sequence 28, Appl
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US-10-142-419-28

US-10-139-262-8

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US-10-012-542-233

US-10-012-542-331
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 31, App
Sequence 31500, A
Sequence 31500, A
Sequence 517, Appl
Sequence 527, Appl
Sequence 5934, Appl
Sequence 5934, Appl
Sequence 77, Appl
Sequence 10236, Appl
Sequence 10236, Appl
Sequence 10236, Appl
Sequence 10236, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 560, Appl
Sequence 55, Appl
Sequence 60, Appl
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CURRENT APPLICATION NUMBER: US/09/872,153
CURRENT FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
SEQ ID NO 22
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-872-153-22
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                                                                                                   Query Match
Best Local S
Matches 171
                                                                                                                                                                                       APPLICANT: Hirst, Shannon K.
APPLICANT: Harlocker, Susan L.
APPLICANT: Dillon, Davin C.
APPLICANT: Walos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.531
                                                                                                                                                                                                                                                                                                       Local Similarity
                                              SMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAV
                            YEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQ
                    YQIQATVMIIVSSCAVAANIVLTVVLHQRCLGHNH----KEVQANASVRAAFVHALGDLFQ
                                                                                                                                                                                                                                                                                                        Conservative
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US-10-175-747-60
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US-10-176-911-60
US-10-176-911-60
US-10-176-911-60
US-10-176-919-60
US-10-176-919-60
US-10-180-543-60
US-10-180-543-60
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US-10-183-010-60
US-10-183-012-60
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Sequence 27, Application US/09957708
Publication No. US20030031678A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Ali, Shujath
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US-09-957-708-27
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Best Local
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CURRENT APPLICATION NUMBER: US/09/957,708
CURRENT FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/233,746
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 40
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GMYRCTIQLQSYRQEVDRTCANCQSSS 428
              HFHTVTIQIEDYSEDM-KDCQACQGPS
                                                              TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLQGKF
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                                                                                                                                                            SGCAVAVNIIMGLTLHOSGHGHSHGTT------NQQEENPSVRAAFIHVIGD
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RESULT 3 US-09-738-626-4910

Sequence 4910, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

NAKAGAWA, SATOSHI

MIZOGUCHI, HIROSHI

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SOFTWARE: PATENTIN VER. 3.0
SEQ ID NO 4910
LENGTH: 318
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Best Local Similarity
            APPLICANT: Kieke, James A.
APPLICANT: Zambrowicz, Brian
APPLICANT: Revelli, Jean-Pierre
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030039962A1el Human
TITLE OF INVENTION: Same
FILE REFERENCE: LEX-0141-IISA
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APPLICANT:
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                    APPLICANT: Walke, D. Wade
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CURRENT APPLICATION NUMBER: US/09/795,927
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                                                                                                                                                                               Wilganowski,
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OCHIAI, KEIKO
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                                                                                                                                                                                 Nathaniel L.
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                                                           Transporter Proteins
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68 GKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRP 127

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                                                                                                       NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for W
SEQ ID NO 2
LENGTH: 507
TYPE: PRT
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                                                                       ; ORGANISM: Human US-09-738-897-2
                                                                                                                                                                                                                                                                                                                                                                                 US-09-738-897-2
                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09738897 Patent No. US20020106721A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 108; Conserv
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LENGTH: 507
Query Match 18. Best Local Similarity 24. Matches 108; Conservative
                                                                                                                                                                                                                                APPLICANT: GUEGLER, Karl et al TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCITTLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CL001053
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/738,897
CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: US 60/185,956
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTTDFASMLISLFSLWMSSRP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GRNRGRLLCMLALTFMFMVLEVVVSRVTSSLAMLSDSFHMLSDVLALVVALVAERFARRT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLVNVLGLCLFHHHSGFSQDSGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDINVAPGEQG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDYSEDMKD----CQ-ACQ 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH---FHTVTIQI 354
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              18.1%;
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71;
Score 347.5; DB 10;
Pred. No. 5.le-27;
1; Mismatches 117;
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US-09-738-897-4
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TYPE: PRT
GRGANISM: Rattus norvegicus
US-09-738-897-4
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Patent No. US20020106721A1
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HID TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CL001053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                            GRNRGRLLCMLLTEMEMVLEVVVSRVTASLAMLSDSFHMLSDVLALVVALVAERFARRT
                                                                                                                                                                                                                                                                                                                                  GKAQRQLYVASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLESLWMSSRP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVEALHSLHIWALTVAQPVLSVHIAIAQNIDAQAVLKTASSRLQGKFH---FHTVTIQI 354
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    VRAAFIHVIGDFMQSMGVLVAAYILYFK-
                                            DQEETNTLVANTSNSNGLKADQAEPEKLRSDDPVDVQVNGNLIQESDSLESEDNRAGQLN 243
                                                                                                                                                                  AVNIIMGLTL--HQS-----GHGHSHG----
                                                                                                                                                                                                           HATQKNTFGWIRAEVMGALVNAIFLTGLCFAILLEAVERFIE-PHEMQQPLVVLSVGVAG 123
                                                                                                                                                                                                                                  -ATKIMNEGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAV 186
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     -TTN----
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24.0%;
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; Pred. No. 9.5e-26;
73; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENCODING HUMAN TRANSPORTER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 507;
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,
PRIOR APPLICATION SEARLIER FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: EARLIER ETILING DATE: 1998-06-16
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; LOCATION: (389)
; OTHER INFORMATION:
US-10-012-542-158
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Publication No. US20030044851A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pa
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
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FILE REFERENCE: PZ029P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (134) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                             RAEVMGALVNAIFLTGLCFAILLEAIERFIE-PHEMQQPLVVLGVGVAGLLVNVLGLCLF 121
                                                                                                                                                                        RAEIIGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTL- 196
                                                                                                                                                                                                                                  ALTEMEMVLEVVVSRVTSSLAMLSDSFHMLSDVLALVVALVAERFARRTHATQKNTFGWI
                                                                  HHHSGFSQDSGHXHSHGGHGHGLPKGPRVKSTRPGSSDINVAPGEQGPDQEETNTLVA
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24.5%;
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Pred. No. 1.3e
57; Mismatches
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Indels 143;

Gaps

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Length

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RESULT 8
US-10-012-542-332
; Sequence 332, Applica
; Publication No. US200
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION UNMBER: EARLIER APPLICATION NUMBER: 09/461,325

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                           ; NAME/REY: SITE ; LOCATION: (403) ; LOCATION: (403) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-012-542-332
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SEQ ID NO 332
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     Matches
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Best Local (
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TITLE OF INVENTION: 94 Human Secreted Proteins
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NAME/KEY: SITE
LOCATION: (148)
OTHER INFORMATION: Xaa
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136 HHHSGFSQDSGHXHSHGGHGHGLPKGPRVKSTRPGSSDINVAPGEQGPDQEETNTLVA 195
                                                 197
                                                                                                                138 RAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTL- 196
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                                                 -HQS------GHGHSHG-----
                                                                                          RAEVMGALVNAIFLTGLCFAILLEAIERFIE-PHEMQQPLVVLGVGVAGLLVNVLGLCLF 135
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                17.3%; Score 333.5; DB 9; 24.5%; Pred. No. 1.3e-25; tive 67; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equals any of the naturally occurring L-amino acids
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_	Qy 303 LHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIEDYSE 359	
	OY 247YKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEA 302	
	Qy 221 FIHVIGDEWQSMGVLVAAYILYFK	
	Qy 213 ENPSVRAA 220	
	QY 187 AVNIIMGLTLHQSGHGHSHGTINQQE 212 : :	
2	Qy 128 -ATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAV 186 : :: : :: ::	
	Qy 68 GKAQRQLYVASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDEASMLISLESLWMSSRP 127 : : : : : : : : : : : : : :	
12;	Ouery Match 17.3%; Score 333; DB 10; Length 503; Best Local Similarity 23.7%; Pred. No. 1.5e-25; Matches 103; Conservative 72; Mismatches 121; Indels 138; Gaps	
	LENGTH: TYPE: PI ORGANISM S-09-738-89	
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PROTEINS,	; PATENT NO. USZUJZUJOK/ZIAI ; GENERAL INFORMATION: ; APPLICANT: GUEGLER, KAR1 et al ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER ; TITLE OF INVENTION: AND USES THEREOF	
	LO IN	
	VPCELACR	
·	376	
	309 WALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTTQIEDYSEDMKD 3	
-	Db 316 YLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQIDIRNLIKELRNVEGVBEVHELHV 375	
	Qy 249 YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHI 308	
_	QY 227 DEMQSMGVLVAAYILYE 248 : : : :	
	Qy 207 -TTNQQEENP	

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420 GSKSSVLPCELACR 433

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PRIOR APPLICATION NUMBER: JP 1
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
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US-10-028-072-28
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US-10-139-262-28
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                                                                                                                     Sequence 28, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
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Best Local :
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CURRENT FILING DATE: 2002-05-07
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APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHOICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                    APPLICANT:
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l Similarity 24.4%;
77; Conservative 7
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                                                                                                    Baker, Kevin P.
              Gao, Wei-Qiang
                               Desnoyers, Luc
Filvaroff, Ellen
                                                                     DeForge, Laura
                                                                                    Beresini, Maureen
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76; Mismatches 124;
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-08-26
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APPLICATION NUMBER: 60/063045
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FILING DATE: 1997-10-17
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                                                 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
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FILING DATE: 1997-11-03
              FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/064248
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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OR FILING DATE: 1998-04-24
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OR APPLICATION NUMBER: 60/08123
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OR APPLICATION NUMBER: 60/081203
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PR APPLICATION NUMBER: 60/074092
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PR APPLICATION NUMBER: 60/069212

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FILING DATE: 1998-01-23
APPLICATION NUMBER: 60/073612
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APPLICATION NUMBER: 60/088026
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                           TASSRLOGKFHFHTVTIQIE 355
                                                                                                                                         QVTGILKDA-GVNNLTIQVE
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ilarity 25.0%;
Conservative
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Pred. No. 9e-20;
6; Mismatches 119;
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; LENGTH: 765
; TYPE: PRT
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US-10-121-049-28
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US-10-121-049-28
; Sequence 28, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
                                  US-10-123-904-28
Sequence 28, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maure,
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellei
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 28
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CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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                                                                                                                                                                                           336 TASSRLQGKFHFHTVTIQIE 355
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                     Baker, Kevin P.
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LENGTH: 765
TYPE: PRT
ORGANISM: Homo S
                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Baker, Ke
                                                                                                                                                                                 Sequence 28, Application US/10140470 Publication No. US20030022331A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                         Baker, Kevin
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Filvaroff, Ellen
                 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L
Sherwood, Steven
                                                              Gerritsen, Mary E
                                                                            Gao, Wei-Qiang
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                                                                                                                         DeForge, Laura
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Pred. No. 9e-20;
6; Mismatches 119;
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; LENGTH: 765
; TYPE: PRT
; ORGANISM: HOMO S
US-10-140-470-28
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 28
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/10175746 Publication No. US20030027270A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
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CURRENT APPLICATION NUMBER: US/10/175,746
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                                                                                        Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Gerritsen, Mary E.
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RESULT 16
US-10-176-918-28
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US-10-176-918-28
                                                SEQ ID NO 28
LENGTH: 765
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 28
LENGTH: 765
TYPE: PRT
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                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C382

CURRENT APPLICATION NUMBER: US/10/176,918

CURRENT FILING DATE: 2002-06-20
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                ORGANISM: Homo
                                 LENGTH: 7
TYPE: PRT
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Wood,William
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Query Match

Length 765;

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; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 550; SEQ ID NO 28; LENGTH: 765; TYPE: PRT; ORGANISM: Homo Sapien
US-10-176-921-28
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US-10-176-921-28
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Best Local Similarity 25.0
Matches 80; Conservative
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Publication No. US20030027276A1
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CURRENT FILING DATE: 2002-06-20
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132 MNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNII 191
                                     417 RQIFYFLCLNLLFTFVELFYGVLTNSLGLISDGFHMLFDCSALVMGLFAALMSRWKATRI 476
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                                                                       72
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                                                          RQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Conservative
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Wood,William
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Filvaroff, Ellen
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                                                                                                        14.5%; Score 278.5; DB 9; 25.0%; Pred. No. 9e-20; tive 76; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 278.5; DB 9; 25.0%; Pred. No. 9e-20;
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                                                                                                          Indels
                                                                                                                                            Length 765;
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	222 IHVIGDEMQSMGVLVAAXILYEKPEVKYVDDICTEVESILVLGTTLTILRDVILVLMEGT 281	γQ
	536 -	Db
	192 MGLTLHQSGHGHSHGTTNQQEENPSVRAAF 221	Qy
	477	Db
	132	Qγ
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9;	Match 14.5%; Score 278.5; DB 9; Length 765; ocal Similarity 25.0%; Pred. No. 9e 20; ocal Similarity 76; Mismatches 119; Indels 45; Ga 80; Conservative 76; Mismatches 119; Indels 45; Ga	
	TYPE: PRT ORGANISM: Homo Sapien -10-137-865-28	us Vs
	NUMBER OF SEQ ID NOS: 550 SEQ ID NO 28 LENGTH: 765	
	PLICATION NUMBER: US/10/137,865 LING DATE: 2002-05-03	· · ·
	TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPERIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C154	
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	APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K	
	APPLICANT: Smith, Victoria APPLICANT: Stewart, Timothy A.	
	APPLICANT: Gurney, Austin L. APPLICANT: Sherwood.Steven	
	APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul J.	
	APPLICANT: Garritsen, Mary E.	
	APPLICANT: Fiveroff; Ellen	
	APPLICANT: DeForge, Laura	
	APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen	·. ··
	GENERAL INFORMATION:	·· ··
	Sequence 28, Application US/10137865	· US
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	36 TASSKLQGKEHEHTVILQIE 3	1 Q
	PPEYEKELHIALEKIQKIEGL	g Db
	PKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLK 3	Qy
		рb
	222 IHVIGDEMQSMGVLVAAXILYFKPEYKYVDPICTEVFSILVLGTTLTILRDVILVLMEGT 281	Qy
	536 -GICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSHGSAG-GGMNANMRGVF 593	Db
	192 MGLTLHQSGHGHSHGTTNQQEENPSVRAAF 221	Qy
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-28
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/10140474 Publication No. US20030032156A1 GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
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CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                     IHVIGDEMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGT 281
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QVTGILKDA-GVNNLTIQVE 727
                             TASSRLQGKFHFHTVTIQIE 355
                                                                   PPEYE----KELHIALEKIQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQ
                                                                                                                                      LHVLADTLGSIGVIVST-VLIEQFGWFIADPLCSLSTAILIFLSVVPLIKDACQVLLLRL
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                                                                                                                                                                                                                                              MGL-----GHGHSHGTTNQQEENPSVRAAF 221
                                                                                                                                                                                                                                                                                 FSYGYGRIEILSGFINGLFLIVIAFFVFMESVARLIDPP-ELDTHMLTPVSVGGLIVNLI
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                                                                                                  PKGVDFTAVRDLLLSVEGVEALHSL-----HIWALTVAQPVLSVHIAIAQNTDAQAVLK 335
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Wood,William
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US-10-142-431-28
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LENGTH: 765
TYPE: PRT
ORGANISM: Homo 9
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                                                                                                   TASSRLQGKFHFHTVTIQIE 355
                                                                                                                                                           PKGVDFTAVRDLLLSVEGVEALHSL-----HIWALTVAQPVLSVHIAIAQNTDAQAVLK
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                                                                                                                                      PPEYE----KELHIALEKIQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQ
                                                                                                                                                                                                                                                                              -GICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSHGSAG-GGMNANMRGVF
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Watanabe, Colin K
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Sequence 28, Application US/10143114 Publication No. US20030036180A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin APPLICANT: Beresini, Ma

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; LENGTH: 765
; TYPE: PRT
; ORGANISM: HOMO S
US-10-143-114-28
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US-10-140-002-28
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: p3330R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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                                                                                                                                             Baker, Kevin P.
 Gurney, Austin L
              Godowski, Paul J.
                                 Goddard, Audrey
                                              Gerritsen, Mary E.
                                                                Gao, Wei-Qiang
                                                                              Filvaroff, Ellen
                                                                                              Desnoyers, Luc
                                                                                                             DeForge, Laura
                                                                                                                              Beresini, Maureen
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Watanabe, Colin K
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Filvaroff, Ellen
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6; Mismatches
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RESULT 23
US-10-142-419-28
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LENGTH: 765
TYPE: PRT
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/10142419 Publication No. US20030044945A1
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               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECR
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or F:
NUMBER OF SEQ ID NOS: 550
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REFERENCE:
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Watanabe, Colin K
Wood, William
                                                             Watanabe, Colin K
Wood, William
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                                                                                              Tumas, Daniel
                                                                                                               Stewart, Timothy A
                                                                                                                                Smith, Victoria
                                                                                                                                                 Sherwood, Steven
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P3330R1C244
             SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
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25.0%;
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Pred. No. 9e-20;
6; Mismatches 1
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Prior Apploication removed - Se
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 28
LENGTH: 765
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-419-28
                                                                                ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 111
; OTHER INFORMATION: Xaa
US-10-139-262-8
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CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
Query Match
Best Local Similarity 24.9
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 8, Application US/10139262
Patent No. US20020128459A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
                                                                                                                                                                                                                           SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                      ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKGVDFTAVRDLLLSVEGVEALHSL-----HIWALTVAQPVLSVHIAIAQNTDAQAVLK 335
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                                14.4%; Score 276.5;
24.9%; Pred. No. 1e-
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                                               Length 594;
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; LOCATION: 537
; OTHER INFORMATION: Xaa
US-10-139-262-10
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US-10-139-262-10
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SEQ ID NO 10
LENGTH: 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1997-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/380, 287A PRIOR FILING DATE: 1999-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/139,262
CURRENT FILING DATE: 2002-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 42
                                                                               NAME/KEY: misc_feature LOCATION: 537
                                                                                                                               NAME/KEY: misc_feature
LOCATION: 514, 528, 565
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                           NAME/KEY: misc_feature
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LOCATION: 339
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ORGANISM: Homo sapiens
                                                                                                                   FEATURE
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OTHER INFORMATION: Xaa
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14.2%;
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Score 272.5; DB 12; Pred. No. 2.6e-19;
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60,

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60,

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-12
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US-10-012-542-233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029P1
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                                                                                                                                                                             LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (134)
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                       138
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                                                                                                      AICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRP-ATKTMNFGWQ 137
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RAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTL- 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKT 131
                                                            ALTFMFMVLEVVVSRVTSSLAMLSDSFHMLSDVLALVVALVAERFARRTHATQKNTFGWI 62
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                                                                                                                                               Score 213.5; DB 9
Pred. No. 9.5e-14;
8; Mismatches 65
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US-10-012-542-331
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Best Local
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NAME/KEY: SITE
LOCATION: (148)
OTHER INFORMATION: >
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1999-12-14
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227 DFMQSMGVLVAAYILYFKPEYK--
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                               NTSNSNGLKLDPADPENPRSGDTVEVQVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLG
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                                                                                                                                                                                          -HQS----
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DATE: 1998-06-22
APPLICATION NUMBER:
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                   YVDPICTFVFSILVL 263
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; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13500
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13500
LENGTH: 394
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                            286 E 286
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                                                                                                                                                                                                             177 YPIVDKLVAIIITFFILKTAYDIFIESSFSLSD----GFDDRLLEDYQKAIMEIPKISKV
                                                                                                                                                                                                                                                                                                                                                                                                                         130 KTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYE-ID--GGTMLITSGCAV 186
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                                                                                                                                                                                                                                                     YKYYDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRD---LLLSVEGVEAL 303
                                                                                                                                                                                                                                                                                                 FVVYLYNTRL-----SKKSNSKALKAAAKDNLSDAVTSLGTAIA--ILASSFN 176
                                                                                                                                                                                                                                                                                                                                         AVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPE 246
                                                                                                                                                                                                                                                                                                                                                                                 RDHRFGHWKIEDLASLITSIIMFYVGFDVLRDTIQKILSREESVIDPLGATLGIISAAIM
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Yamamoto, Robert T.
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Zyskind, Judith W.
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18.6%; pre/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 132; DB 10;
Pred. No. 2.6e-05;
9; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                         RESULT 30
US-09-823-114-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                         Sequence 21, Application US/09823114
Patent No. US20020061554A1
GENERAL INFORMATION:
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LENGTH: 286
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                             228 IDRLRLRWVGHRLHGDA-TVSTSTSSLSEATAIALEAELSVK
                                                                                                                                                                                                                                                                                                                                                                                                   300 VEAL-----HSLHIWALTVAQPVLSVHIAIAQNTDAQAVLK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ATQKYTYGFNRAEDLAGLFIVAMIALSAIVAAWQAIDRMINPRPMENIEWVIAAGVIGFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 RQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLW----MSSRP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 RALKFSLVLMLLTTVLQAIIVSFSGSVALLADTVHNLSD----ALTAIPLWIAFILSRRA 64
                                                       TITLE OF INVENTION: OPIOID RECEPTOR GEI
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE,
                                                                                                                                                                   APPLICANT: EVANS, CHRISTOPHER J. KEITH, DUANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                             FL--GFPLADPIIGLIISAMIATLLVGTIRSVGRRLMDGIEPELVEKATHAIWHVKEIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNEAVAMYRI------RVGKRIGSAALVADGVHARTDGFTSLAVVAGGVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYIL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISG------DYEIDGGTMLIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
COUNTRY: USA
                   STATE: DC
                                     CITY: WASHINGTON
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OZAKI, AKIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOKOI, HARUHIKO
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Length 286; Indels

40;

Gaps

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299 169

RESULT 29

ZIP: 20006-1888

Suite 5500

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NAME/KEY: Modified-site

LOCATION: group(18, 33)

OTHER INFORMATION: /note- "extracellular Asn residues;
that are consensus sites for N-linked glycosylation"

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-823-114-21
                                                                  RESULT 31
US-09-738-626-3686
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Sequence 3686, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     311 LN------PVLYAFLDENFKRCFRQLCRKP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                    341 LQGKFHFHTVTIQIEDYSEDMKDC--QACQGP 370
                                                                                                                                                                                                                                                                                                                                         174 LASGYGVPI-MVMAVTRPRDG-----
                                                                                                                                                                                                                                                                                                                                                                                                          114 PFGELLCKAVLSIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 PLPRPGLDLQAIELAAQSNHHCHA--QKGPDSHCDPKKGKAQRQLYVA-----SAICLLF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 MIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNF------GW 136
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REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                        QRAEIL-GALVSV-----LSIWVVTGVLV--YLAVERLISG-DYEIDGGTMLI-----
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                                                                                                                                                                                                                                     RDLLLSVEG--VEALHSLHI----WALTVAQ----PVLSVHIAIAQNTDAQAVLKTASSR 340
                                                                                                                                                                                                                                                                       LQFPSPSWYWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRI
                                                                                                                                                                                                                                                                                                                                                                       -TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGNVL------VMFGIVRYTKMKTATNIYIFNLALADALATSTLPFQSAKYLMETW
                                                                                                                                                                                                      TRMVLVVVGAFVVCWAPIHIFVIVWTLVDIRRDPLVVAALHLCIA----
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%; Score 100.5; DB 10; 21.2%; Pred. No. 0.038;
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 REFERENCE:
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RESULT 32
US-09-738-626-5835
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Sequence 5835, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Pate
SEQ ID NO 3686
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APPLICANT:
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                                                                                      APPLICANT:
                       APPLICANT:
TITLE OF II
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 458
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 VRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 YEIDGGTMLITSGCAVAVN---IIMGLTLHQSGHGHSHG-----TTNQQEENPS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 FTLLFQVAFGWS-ATLAGAMVVALFAGNVAIKPFTTPIIKRWNFKPVLVFSNA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 NTAVNVKRFDLPGFLGAMLVMVALTVAAEL----ISRGSSAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 DPKDLLDAIAFLTWPALVAPVIAPLLGGLLADTIGWRWIFLLNVPLGIIAIIAGLFILPK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 VLSATLHQLG---MSLGIAVAVIAMSLAPTANWAFPLAAALFLIPLIG-ALSLPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTM----NFGWQRAEILGALV------SVLSIWVVTGVLYYLAVERLISGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACLV-LSAAVVCGFVVRWLRV----PGRLFDLSIMRIPGFRVGNSSGSIYRLVITAAPFM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PG-----LDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKQHLLDA-----RPAIRSYTGSLWQEGAGW-----IP-----LPR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AGALVLATFLFVRADTPLVLIVLLLFVSGALRSLGFSAYNTLQFVDISPEQTSNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
INVENTION: NOVEL POLYNUCLEOTIDES ERENCE: 249-125
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                  NAKAGAWA, SATOSHI
                                         IKEDA, MASATO
OZAKI, AKIO
                                                                                      TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                       OCHIAI, KEIKO
                                                                                                                                    YOKOI, HARUHIKO
                                                                                                                                                                                                        ANDO, SEIKO
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ANDO, SEIKO
                                                                                                                                                                              HAYASHI,
                                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
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                                                                                                                                                                                   MIKIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99.5; DB 9; Length 458; Pred. No. 0.064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLFSLWMSSRPAT 129
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PAtentin ver. 3.0
SEQ ID NO 5835
LENGTH: 306
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5835
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                                         δÃ
                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Homo sapiens US-10-112-599A-4
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US-10-112-599A-4
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Publication No. US20030005476A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D
TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING THERETO
FILE REFERENCE: R-678
CURRENT APPLICATION NUMBER: US/10/112,599A
CURRENT FILING DATE: 2002-09-05
                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 372
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Best Local (
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                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 MISVSIPMVIVGRVKINLAKDLHDK----------LLYADADMAKADWG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 WORAEILGALVSVLSIWVVTGVLVYLAVERLISGD-----YEIDGGTMLITSGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 KHRSIAIGHQAAALALLIMGSLLIYEAVSALIKGERPPIGLAILFGHDVWSGWLMI--GV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 IAWVLFSIVLVGVVAGQSQAMRSAWIEDMLSLVPPIAFLLASR----ISKAVATRKHPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 VASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 62; Conserv
                                         32 PLPRPGLDLQAIELAAQSNHHCHA--QKGPDSHCDPKKGKAQR-QLYVA-----SAICLL 83
                                                                                         Local Similarity 21.3 les 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRL--QGK-FHFH 348
PAPSAGAELQPPLFANASDAYPSAFPSAGANASGPPGPGSASSLALATATTALYSAVCAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLNDDVE -- KAALEMH-W-----
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                                                                                       4.9%; Score 93.5; DB 9; Length 372;
21.3%; Pred. No. 0.19;
ative 57; Mismatches 138; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 94.5; DB 9; Length 306; 20.0%; Pred. No. 0.12; tive 53; Mismatches 114; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VKHARARIRDQGRCFHTE 258
                                                                                       Indels 115;
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	200	QY 142 LGALVSVLS-IWVVTGVLVYLAVERLISGDYBIDGGTMLITSGCAVAVNIIMGLTLHQSG	
	141 303	Qy 85 MIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWM-SSRPATKTMNFGWQRAEI :: : : : : : : : : : : : : : : : : :	
	84 244	Qy 32 PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLF	
16;	Gaps	Query Match 4.8%; Score 93; DB 9; Length 441; Best Local Similarity 23.9%; Pred. No. 0.28; Matches 65; Conservative 47; Mismatches 90; Indels 70; Ga	
		; TYPE: PRT; ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5934	
		SES	
		PRIO	
		PRIOR FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: JP 00/1591	
		CURREN	
		TITLE OF INVENTION: NOVEL POLYNUCLEOTIDE FILE REFERENCE: 249-125	
		APPLICANT:	
		APPLICANT: YOKOI, APPLICANT: TATEISH	
		APPLICANT: APPLICANT:	
		; APPLICANT: MIZOGUCHI, HIROSHI ; APPLICANT: MIZOGUCHI, HIROSHI	
		RESULT 34 US-09-738-626-5934 ; Sequence 5934, Application US/09738626 ; Publication No. US20020197605A1 ; CENERAL TURORMATION:	
		Db 311 SSLNPVLYAFLDENEKRCFRQLCRKP 336	
		MKDC QA	
	-	:: : : : : : : : :	
	338	OV 290 VRDLILSVEGVEALHSLHTWALTVAOPVLSVHTAIAONTDAOAVLKTAS	
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	198	Db 174 VLASGVGVPI-MVMAVTRPRDGAVVC	
	238	QY 181TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAA	
	173	Db 114 WPEGELLCKAVLSIDYYNMETSIETLTMMSVDRYIAVCHPVKALDERTPAKAKLINICIW	
	180	;	
	113	Db 63 GLLGNVLVMFGIVRYTKMKTATNIXIFNLALADALATSTLPFQSAKYLMET	
	135	GYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFG	

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US-09-510-332-77
US-09-510-332-77
Sequence 77, Application US/09510332
Publication No. US20030022278A1
GENERAL INFORMATION:
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                                                                                                                                                     US-09-393-634-1
                                                                      Sequence 1, Application US/09393634 Patent No. US2002005.1997A1 GENERAL INFORMATION: APPLICANT: Zuker, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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SEQ ID NO 77
LENGTH: 335
                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278A1el Family of Taste Receptors
FILE REFERENCE: 02307E-098010US
CURRENT APPLICATION NUMBER: US/09/510,332
CURRENT FILING DATE: 2000-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
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 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 TIPHPLFLWLKMRI-----SRLVPWLILGSVLYVIITTFI---HSRETSAILKPIFISLF 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 N-----FGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTML-----
                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                  161 PKNATQVGTGHATLLSVLVLGLTLPLFIFTVAVLLLIYSLWNYSRQMRTMVGTREYSGHA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 LCILFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 ICLLFMIGEVVGGYLAHSLAVMTDAAHLLTD-----FASMLISL-FSLWMSSRPATKTM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 59; Conserv
                                                                                                                                                                                                                                                                                                                                           HSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PICTFVFSILVLGTTLTI-LRDVILVLMEGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGHSHGTTNQQEENPSVRAAFIHV--IGDFMQSMGVLVAAYILYFKPE-----YKYVD 251
                                                                                                                                                                                                                              IGMYPSI-HSIVLIL--GNPK-----LKRNAKMFIVHCKCCHCTRAW-VTSRSPRLS
                                                                                                                                                                                                                                                                  LGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLS 319
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Adler, Jon Elliot
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                                 Zuker, Charles S.
Adler, Jon Elliot
Ryba, Nick
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Mueller, Ken
Hoon, Mark
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19.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91; I
Pred. No. 0.
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US-09-966-871-80
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Вb
                                                                                                                                                        ; ORGANISM: Homo US-09-966-871-80
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KOpin, Alan S.
TITLE OF INVENTION: Assays for Identifying Receptors Having
TITLE OF INVENTION: Alterations in Signaling
FILE REFERENCE: 00398/512002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 80\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/966,871 CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: US 60/236,302 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US 60/288,644 PRIOR FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 199-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 ICLLFMIGEVVGGYLAHSLAVMTDAAHLLTD-----FASMLISL-FSLWMSSRPATKTM 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIPHPLFLWLKMRI-----SRLVPWLILGSVLYVIITTFI---HSRETSAILKPIFISLF 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGMYPSI-HSIVLIL--GNPK-----LKRNAKMFIVHCKCCHCTRAW-VTSRSPRLS
                                 PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCD-PKKGKAQRQLYVA-----SAICLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISAML -----SILSFLILYLSHYM -- VAVLISTQVLYLGSR -----TFVFCLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILV 262
PAPSAGAELQPPLFANASDAYPSACPSAGANASGPPGARSASSLALAIAITALYSAVCAV 62
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                                                                                                 Similarity
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19.98;
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                                                                          Score 89.5; DE Pred. No. 0.5; 60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 10;
Pred. No. 0.3;
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                                                                                Indels
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APPLICANT: KOPIN, Alan S.
APPLICANT: KOPIN, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: Constitutively Active, Hypersensitive,
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE,
TITLE OF INVENTION: And No. US20020147170Aifunctional Receptors as No. US20020147170
FILE REFERENCE: 00398/510002
CURRENT APPLICATION NUMBER: US/10/039,645
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/243,550
PRIOR FILING DATE: 2000-10-26
NUMBER: OF SEQ ID NOS: 87
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-645-80
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US-10-039-645-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                        199 MLQFPSPSWYWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRR 258
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  290 VRDLLLSVEG--VEALHSLHI----WALTVAQ-----PVLSVHIAIAQNTDAQAVLKTAS
                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                        84 FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNF------G
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                                                                                                                  VLASGVGVPI-MVMAVTRPRDG-----AVVC
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                                                                                                                                                        --TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAA 238
                                                                                                                                                                                                                                  WQRAEIL-GALVSV-----LSIWVVTGVLV--YLAVERLISG-DYEIDGGTMLI-----
                                                                                                                                                                                                                                                                          GLLGNVL------VMFGIVRYTKMKTATNIYIFNLALADALATSTLPFQSAKYLMET 113
                                                                                                                                                                                                                                                                                                                                                  PAPSAGAELOPPLFANASDAYPSACPSAGANASGPPGARSASSLALAIAITALYSAVCAV 62
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                                                                            YILYFKPEYKY - - VDPICTFVFSILVLGTTLTILRDVILV - - - - - LMEGT - PKGVDFTA 289
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US-09-815-242-10236
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US-09-815-242-10236
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LENGTH: 412
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APPLICANT:
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  262
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  VLGT -
                                                                          VIGDFMQSMGVLVAAYILYFK----
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Similarity 19.9%;
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Yamamoto, Robert T.
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Zyskind, Judith W
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TLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGV 300
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
244 TIAGFVNLAMMATAAAAFHFSGHTGVADLDEAYLTLQPLLSHAAATVFGLSLVAAGLSST 303
                                                                                                                     184 KGMVIPSLPTSEAVFLAAGVLGATIMPHVIYLHSSLTQHLHGGSRQQRYSATKWDVAIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 DPKKGKAQRQLYVA-SAICLLFMIGEVVGGYLAHSLAVMTDAAHLL-----TDFASMLI 116
                                                                                                                                                                             GTMLI----TSGCAVAVNIIMGLT-----LHQSGHGHSHGTTNQQEENPSV-RAAFIH 223
                                                                                                                                                                                                                                          LGVSLLQGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELIFSQPNLAQLG
                                                                                                                                                                                                                                                                                                         --VSVLSIWVVTGVLVYL------AVERLISG------DYEID-------G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATNIQAGASFGYQLLWVVVWANLMAMLI
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Pred. No. 0.64;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTMARE: PATENTIN Ver. 3.0
SEQ ID NO 4772
LENGTH: 513
TYPE: PATE
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4772
Search completed: March 18, 2003, 15:46:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4772, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                    183 FPHAVAGGFLTAGTFVLGISGWWIIRAHRQAKKAESEIESKHSMHRPALWVGWWTTVVSS 242
                                                                                                                                                                                                                                                                                                                                                          123 WLHTASIWIVAIATNISAYFIIVANSFMQHPVGAEYNPETGRAELTDFWALLTNSTALAA 182
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SENOH, AKIHIRO
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HAYASHI, MIKIRO
OCHIAI, KEIKO
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A;Gene: ZnT-2
A;Start codon:
C;Superfamily:
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$70632

zinc transporter ZnT-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence_revision 10

C;Accession: $70632
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Palmiter, R.D.; Cole, T.B.; Findley, S.D. EMBO J. 15, 1784-1791, 1996
A;Title: ZnT-2, a mammalian protein that co A;Reference number: S70632; MUID:96203098; A;Accession: S70632
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-359 <PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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Best I
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                                                                            AIRSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQL
                                             LTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQGP
                                                                                                                           ALHQSGHGHSHGHSHEDSSQQQQNPSVRAAFIHVVGDLLQSVGVLVAAYIIYFKPEYKYV
                                                                                                                                        YVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLIDFASMLISLFSLWMSSRPATKTMNF
                                                                                                                                                                                                                                                                       ASRSFFGALWKSEASRI----PPVNLPSVELAVQSNHYCHAQKDSGSHPNSEKQRARRKL
         SD
                                                                                                                                                                                                                       YVASAICLVFMIGEIIGGYLAQSLAIMTDAAHLLTDFASMLISLFSLWVSSRPATKTMNF
                                LTVAQPVLSVHIAIAQNVDAQAVLKVARDRLQGKFNFHTMTIQIESYSEDMKSCQECQGP
            372
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                                                                                                                                                                                                                                                                                                                             77.6%;
80.1%;
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                                                                                                                                                                                                                                                                                                                   35; Mismatches
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AB2671
C81049
T23089
T47777
C83703
T21751
S58449
S74951
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$75795
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                                                                                                                                                                                                                                                                                                                               Score 1493; DB 1;
Pred. No. 4.5e-119;
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                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAB02775.1; PID:g1256378
                                                                                                                                                                                                                                                                                                                                         Length 359;
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hypothetical
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protein F309.11 [i
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                                                                                                                                                             hypothetical protein Y39E4A.2b - Caenon C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision C; Accession: T26757 R; Barlow, K.
                                                                                                                                                                                                                       RESULT 3
T26757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T18D3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T24963

R;McMurray, A.

R;McMurray, A.

R;McMurray, A.
                                                                                          A; Molecule type: DNA
A; Residues: 1-410 <WIL>
                                                                                                                           submitted to the EMBL Data A; Reference number: Z20260 A; Accession: T26757
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A; Residues: 1-382 <WIL>
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                       A; Gene: CESP: Y39E4A.2b
A; Map position: 3
A; Introns: 97/3; 362/1
                                                                   A; Cross-references: EM
A; Experimental source:
                                                                                                                A; Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                   EMBL:AL021480;
ce: clone Y39E41
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                                                                                                                  translated
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48.6%; Pred. No. 1.8e-63;
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 Score
                                                                                PIDN:CAA16328.1;
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  410;
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hypothetical protein Y39E4A.2a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex: C;Accession: T26756 R;Barlow, K. submitted to the EMBL Data Library, January 1998 A;Reference number: Z20260 A;Accession: T26756
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A;Experimental source: clone Y39E4A
C;GenetLcs:
A;Gene: CESP:Y39E4A.2a
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A; Residues: 1-391 <WIL>
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Best Local Similarity
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                                                                                                                                                                                                            QSLAIMTDAGHMLSDLLSFIISIFAIRCARLPASKRLSFGYERAEVLGALTSVIILWVLT
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DAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQ
                               VMRDIFFVLMEATPSHYDLSDVKKALSALEGVKGVHDLHLWSIGMDKTAFSVHLALESPN
                                                AHDGKNVNVRAALIHVIGDLVQSIGVLIAALIIRF-TGWTLADPICTFLFSIIVLFTTVT
                                                                                                       -QQEENPSVRAAFIHVIGDFMQSMGVLVAAYILVFKPEVKYVDPICTFVFSILVLGTTLT
                                                                                                                                                 TVLVVVAIQRIVNNEHEVDADVMLITAGVGVLFNIVMGLVLHFGTGGHGHTHGGHSSHGH
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3; Mismatches 104;
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Pred. No. 7e-52;
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RESULT 6
T49164
zinc transporter-like protein - Arabidopsis thaliana
N;Alternate names: protein T20N10.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #
C;Accession: T49164
C;Accession: T49164
C;Accession: T49164
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A; Map po
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; T
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalian
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84907
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A; Accession: T02681
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A; Residues: 1-398 <STO>
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A; Residues: 1-398 < R
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Best Local Similarity
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37.9%;
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L.; Tallon,
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sis thaliana (mouse-ear cress)
#sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

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G.;

Mewes,

H.W.;

Rudd,

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N;Alternate names: protein F21F14.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 27-Nov-2001
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A;Residues: 1-378 <DAN>
A;Residues: 1-378 <DANS
A;Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.160
A;Experimental source: cultivar Columbia; BAC clone T20N10
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A; Reference number:
A; Accession: T49164
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A; Note: F21F14.110
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A; Residues: 1-334 <CHO>
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A; Accession: T47986
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C; Accession: T47986
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Best Local 9
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                                                                              SHCDPKKGKA-QRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLF 119
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SLWASSWEANPROSYGFFRIEILGTLVSIQLIWLLTGILVYEAVTRLVQETNDDVDGFFM
                                                                SSSDAKKRAASMRKLCFVVVLCLLFMSIEVVCGIKANSLAILADAAHLLTDVGAFAISML
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                                                                                                                                    Conservative
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                                                                                                                                    Mismatches 105;
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RESULT
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probable zinc transporter [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) (;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (;Accession: A84696 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; I
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A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 29.8 es 114; Conservative
                                                                         FGILMERVPRDMDIEKLERGLKRIDGVKIVYDLHVWEITVGRIVLSCHILPEPGASPKEI
                                                                                                                                                                           RNSFGFKRLEVLAAFLSVQLIWLVSGVIIHEAIQRLLSRSREVNGEIMFGISAFGFFMNL
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                                     LKTASSRLQGKFHFHTVTIQIE 355
                                                                                                           ILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAV
                                                                                                                                                   NINIQGAYLHAMADMIQSLGVMIGGGIIWVKPKWVLVDLICTLVFSAFALAATLPILKNI
                                                                                                                                                                                                                             VMVLWL---GHNHSHHHHDHHHHHHHHHHHHKHQHQHHHKEVVAEEEEEEMNPLKGEKSSSKEM
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ITGVRNFCRKSYGIYHATVQVE 383
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Pred. No. 8.7e-35;
1; Mismatches 130;
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RESULT 10
H64810

ybgR protein - Escherichia coli (strain K-12)

C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: H64810
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A.;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cation transport protein ybgR [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AE0993
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.S.
                                                                                                    A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-313 <BLAT>
A;Cross:references: GB:AE000177; GB:U00096; NID:g1786955; EA;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
A;Title: Complete genome sequence of a multiple
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0593
A;Status: preliminary
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A; Residues: 1-312 < PAR>
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                                                                                                                                                                                                          A; Accession: H64810
    ;Superfamily: zinc transporter ZnT-2;Keywords: transmembrane protein;21-37/Domain: transmembrane #status
                                                                                Genetics:
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  #status
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Pred. No. 5.4e-29;
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  predicted
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292 169 233 119

EGGMMMAIAVAGLLANILSFWLLH------HGS---EEKNLNVRAAALHVLGDLLGSVG

MLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEI 173

LLFALLAVQFSRRPPTIRHTFGWLRLTTLAAFVNAIALVVITILIVWEAIERFRT-PRPV

DGGTMLTTSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFTHVIGDFMQSMG

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transport system permease protein ECs0780 [imported] - Escherichia coli (str C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: D90726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:54-70/Domain: transmembrane #status predicted <TM2>F:90-106/Domain: transmembrane #status predicted <TM3>F:126-142/Domain: transmembrane #status predicted <TM4>F:164-180/Domain: transmembrane #status predicted <TM5F:188-204/Domain: transmembrane #status predicted <TM5F:188-204/Domain: transmembrane #status predicted <TM5F:188-204/Domain: transmembrane #status predicted <TM6F:188-204/Domain: transmembrane #status predicte
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C; Accession: G82752
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R; anonymous, The Xylella fastidiosa Consortium of the Organization for R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A: Note: for a complete list of authors see reference number A59328 bel
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A; Residues: 1-311 <STO>
A; Cross-references: GB: AE005174; NID: 912513681; P
A; Cross-references: strain 0157: H7, substrain
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Date: 16-Feb-2007
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Pred. No. 1.2e-28;
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A;Gene: SCOEDB:
C;Superfamily:
                                                                                                                                                                                                                                 R;Oliver, K.; Harris, D.; Bentley, S.D.; submitted to the EMBL Data Library, April A; Reference number: Z21573
A;Accession: T35276
A;Status: preliminary; translated from GB A;Molecule type: DNA A;Residues: 1-312 <OLID
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Best Local S
Matches 98
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                                                                                                                        SCOEDB: SC5F2A.34c
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Rerreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, C.R.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Niveira, M.C.; de Salva, A.; Santellii, R.V.; Sawa, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.; Santellii, R.V.; Sawa, A.; Santellii, R.V.; Santellii, R.V.; Sawa, A.; Santellii, R
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                                 probable efflux protein - Streptomyces C;Specias: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision C;Accession: T35276
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A; Residues: 1-321 <SIM>
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A; Status: preliminary
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C;Superfamily: zinc transporter
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98; Conser
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Pred. No. 3.6e-28;
4; Mismatches 126
                                                                                          05-Nov-1999
                                                                                                                                                                                coelicolor
Parkhill,
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transporter ZnT-2

PIDN: CAB40701.1;

GSPDB:GN00070; SCOEDB:SC5F2A.34c

GB/EMBL/DDBJ

. 78;

Score 416.5;

DВ

2

312;

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RESULT 15
AG1396
Cation transport protein (efflux) homolog lmo2575 [imported] - Listeria monocyto C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1396
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-303 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00653.1; PID:g16412063; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
C;Gene: lmo2575
C;Superfamily: zinc transporter ZnT-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1396
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                           LLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERL
                                                   DLLGSVGAIIAALLIIFL-GWNIADPIASVIVAALILVSGWRVLKDAIHILMEGKPANVD
                                                                                           DFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVD
                                                                                                                                                                              ISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIG
                                                                                                                                                                                                                                                                                                                        AHNHDHAHGHNHNHAHNANKK-----SLFISFILIATFMVVEVIGGIMTNSLALLSDAGH
                                                                                                                                                                                                                                                                                                                                                                   AQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAH 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KFHFHTVTIQIEDYSEDMKDCQACQ 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSR----LQG---
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       FTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH 346
                                                                                                                                        FDPPQVIGAGMMTI-SVIGLLINILVAWILMK-----GDTS---ENLNMRSAFLHVLG
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                                                                                                                                                                                                                                                                                                                                                                                                           21.6%; Score 414.5; DB 2; Similarity 30.1%; Pred. No. 1.3e-27; 93; Conservative 72; Mismatches 127;
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hypothetical protein SA0163 [imported] - Staphylococcus aureus (strain N315 c;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: D89778 T; Uchiyama, I; Baba, T; Yuzawa, H.; Kobayashi, I; (ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sc.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureu A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                 D89778
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C;Genetics:
A;Gene: lin2720
C;Superfamily:
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A; Molecule type: DNA
A; Residues: 1-303 <GLA>
A; Cross references: GB:AL592022; PIDN:CAC97946.1;
A; Cross references: Strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB1772
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
C;Accession: AB1772
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LEHSTIQLE
                                                                                                                                              TEEIKTFFQQQDGVKEVHDLHVWAITSDFNALSAHLTVCEDADRDKILADIEHYLQENFS
                              FHTVTIQIE
                                                                                                                                                                                            FDPPQVIGAGMMTI-SVIGLLINILVAWILMK------GDTS---ENLNMRSAFLHVLG
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                                                             TEEIKTFFQEQDGVTEVHDLHVWAITSDFNALTAHLTVAEDADRDKILTDIEHYLQENFS
                                                                                           FTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH
                                                                                                                             DLLGSVGAITAALLIIFF-GWNIADPIASVIVAALILVSGWRVLKDAIHILMEGKPANVD
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Pred. No. 2.
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?.9e-27;
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Dussurget, O.; Entian, K.D.;
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; Cui, L.; Sekimizu,

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A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumsteln, E.; Yoshikawa, H.; Danchin, A.
A; Tutle: The complete genome seguence of the Gram. positive bacterium Bacillus subtilis. A; Accession: C69612
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A;Gene: SA0163
C;Superfamily: zinc transporter ZnT-2
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-319 < KUR>
A; Cross-references: GB:BA000018;
A; Experimental source: strain N31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                            A;Cross-references: GB:Z99117; GB:AL009126; A;Experimental source: strain 168
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-311 <KUN>
                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bes
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MADIKNIDGILDVHEFHLWSITTEHYSLSAHVVLDKKYEGDDYQAI-DQVSSLLKEKYGI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPIESGIMFMIASIGLLVNIILTIILVRS-----LKQEDNINIQSALWHFMGDLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQ
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93; Conserv
Similarity
                                                                       zinc transporter ZnT-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %; Score 399.5; 1
%; Pred. No. 2.6e
84; Mismatches
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  Score
Pred.
  397.5; DB 2; No. 3.8e-26;
                                                                                                                                                                  NID:g2634966;
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                           311;
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                                                                                                                                                                                                                                         not shown
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M.; Chd
Lri, E.
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
A;Accession: AH3431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-301 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52619.1; PID:g17983439; GSPDB:GN00190
A;Experimental source: strain 16M
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C; Superfamily: zinc transporter ZnT-2
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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Matches
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 93; Conserv
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                                                                                                                                                                                                                                     SLFSLMWSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGG
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                                                                                       TMLITSGCAVAVNIIMG--LTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGV 234
                                                                                                                                                                                                                ALIAIYLGRRPADVLRTYGYARFEILAAAFNALLLLGVAFYILYEAWERL-SEPADVQSL
                                                                                                                                                                                                                                                                                       GADHEHADVKNTPISR-LWIAFGLTGIFMIAEVIGSFATGSLALLSDAMHMATDAFALLL
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LAVPGVASVHDLHVWSLTKTEHSLTAHLVLAQEADGETVRRAVEHVLQNDYDLHHTTLQT 289
                               LSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQI 354
                                                                     IAAAIIIYL-TGWEWVDSAIAVGIGFMVFPRTWVLLKECINILLEGVPAGGDVKKLEAAI
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                               20.5%; Score 393.5; DB: 30.9%; Pred. No. 7.9e-26
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                                                                                                                                               -KDDSLNVKGAYLEVWADMLGSVGV
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RESULT 21
T44365
Cation-efflux system membrane protein homolog [imported] - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Apate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
C;Accession: T44365
R;Kuroda, M.; Hayashi, H.; Ohta, T.
Microbiol. Immunol. 43, 115-125, 1999
A;Title: Chromosome-determined zinc responsible operon czr in Staphylococcus aureus sA;Reterence number: Z22754; MUID:99244271; pMID:10229265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-325 <KUR>
A;Cross-references: EMBL;AB016431; PIDN:BAA36686.1
A;Experimental source: strain 912
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-325 <KUR>
A;Cross-references: GB:BA000018; PID:g13701940; PIDN:BAB43232.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: czrB
C;Superfamily: zinc transporter ZnT-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: G90008
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                               DLLHLNIHHMTIQLETPNHKHDESIICSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHSHHHDHMH----SHVTTNNKKV---LFISFLIIGLYMFIEIIGGLLANSLALLSDGIH 54
                                                                                                                                                                                                                                                                                                                                                                                                IDEVITTIKKDSRIQSVHDCHVWTISNDMNALSCHVVV----DHTLTMKECELLLENIEH
                                                                                                                                                                                                                                                                                                                                                                                                                              FTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFSDTFSLGVALVAFIYAEKNATTTKTFGYKRFEVLAALFNGVTLFVISILIVFEAIKRF 114
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                                                                                                                                      Staphylococcus aureus
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C.; Sekimizu,
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A; Residues: 1-316
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Best Local
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A; Note: czrB
C; Superfamily: zinc transporter ZnT-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 IHMFSDTFSLGVALVAFIYAEKNATTTKTFGYKRFEVLAALFNGVTLFVISILIVFEAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SHSHHHDHMH----
                                          FH----FHTVTIQIEDYSEDMKDCQACQG 369
                                                                                                                           VDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGK 344
                                                                                                                                                                                                                                                                                              RLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHV
EHDLLHLNIHHMTIQLETPNHKHDESIICSG
                                                                                  VDIDEVITTIKKDSRIQSVHDCHVWTISNDMNALSCHVVV---
                                                                                                                                                                   IGDLLGSVGAITAA-ILIWAFGWTIADPIASILVSVIILKSAWGITKSSINILMEGTPSD
                                                                                                                                                                                                                IGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKG
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97; Conserv
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;; Pred. No. 1.7e-25;
73; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325
                                                                                     DHTLTMKECELLLENI
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R;Kunito, T.; Kusano, T.; Oyaizu, H.; Senoo, K.; Kanazawa, S.; Mats Biosci. Biotechnol. Biochem. 60, 699-704, 198 for A;Title: Cloning and sequence analysis of czc genes in Alcaligenes A;Reference number: JC4698; MUID:96219090; PMID:8829543 C;Species: Alcaligenes sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4701 A;Gene: czcD C;Superfamily: zinc transporter ZnT-2 A; Cross-references: DDBJ:D67024 121 LWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLI 180 61 SHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFS 120 Local Similarity TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYI SHDHP--GGNERSLKIALALTGTFLIAEVVGGVMTKSLALISDAAHMLTDTVALAIALAA 63 KSFHDLHIWALTSGKASLTVHVVNDTAVNPEME-VLPELKQMLADKFDITHVTIQFE EALHSLHIWALTVAQPVLSVHIA - - IAQNTDAQAVLKTASSRLQGKFHFHTVTIQIE 355 IRF-TGWAWVDSAIAVLIGLWVLPRTWFLLKSSLNVLLEGVPDDVDLAEVEKQILATPGV LYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGV VAVLGLIINLI-SMRMLSSG------QSSSLNVKGAYLEVWSDLLGSVGVIAGAII IAIAKRPADKKRTFGYYRFEILAAAFNALLLFGVAIYILYEAYLRLKSPP-QIESTGMFV cobalt divalent cation resistant determinant D - Alcaligenes Conservative <KUN> 20.1%; %; Score 387; DB 1 %; Pred. No. 3e-25; 57; Mismatches 1 DB 1; 120; Length 316 Indels S.; Matsumoto, 18; sp. 286 Gaps 300 230 171 240 122 strain ďs 7; CT14

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RESULT 24
F87286
F87286
Cation efflux family protein [imported] - Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C. Accession: F87286
                                 A;Cross-references: GB:AE005673;
C;Genetics:
A;Gene: CC0303
                                                                                                                                  R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: F87286
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C; Super:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cation transport protein YPO1129 [imported] - Yersinia pestis (str:
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AI0138
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AI0138
                                                                                   A; Molecule type: DNA
A; Residues: 1-361 <STO>
                                                                                                                      A;Status: preliminary
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A; Residues: 1-312 < KUR>
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Best Local S
Matches 92
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                                                                                                                                                                                                                                                                                                                                                                                                   PAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILSVLVSVLILRSAWRLLKESFHELLEGAPQEIDINKLRKDLCTNIYEVRNIHHVHLWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNFGWORAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNII 191
                                                                                                                                                                                                                                                                                                                                                                                                                                   372
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   19
                                                                 NID:g13421446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAC89972.1;
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore 380.5; DB 2;
ed. No. 1.1e-24;
Mismatches 125;
   374.5;
   DВ
                                                                     PIDN:AAK22290.1; GSPDB:GN00148
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 2:

    Yersinia pestis (strain

Length
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                                 I-AQNTDAQAVLKTASSRLQGKFHFHTVTIQIE
                                                                                                 GTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIA 323
                                                                                                                                                      FLVAEVVGGILTGSLALISDAAHMLTDAVALAIALAAINIARRPTNDRLTYGYHRFEILA
 YDPALVDAEALLGTVKALLHDRYEIEHSTLQLE
                                                                   PRIWILLRESTHYLLEGYPKEIQLAELREALLGIPGYTGLHDLHVWSITSGKISLTSHLV
                                                                                                                                      S-----TINVKGAYLEVWSDMLGSLGVIVAAIVIRF-TGWAWVDSLVAVLIGFWVL
                                                                                                                                                                                                        AAFNAFLLFGVAFYILYAAYERL-NQPAEIQSVGMLVIAVLGLLVN-LASMRLLAPAQGN
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Best Local Similarity Matches 92; Conser
                                              TVTIQIEDYSEDMKDCQACQ-GPSD 372
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HVTIQV----ESGHGAHACRLAPAD
                                                                                                                                                   AVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFH
                                                                                                                                                                                                    VSAGVVIAALAMTF-TGWMWLDPVVSLVIVAVIVLG-TWGLLRDSLDLALDATPRGIDTQ
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                                                                                                  KVRDWLAARPGVSEVHDLHIWAMSTTETALTAHVVRQLDADHDQFLHDACAELASRFNIG
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0; Mismatches 140;
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A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE004477; GB:AE004091; NID:g99946248; PIDN:AAG03786.1;
A;Cross-references: GB:AE004477; GB:AE004491; NID:g99946248; PIDN:AAG03786.1;
A;Cross-references: GB:AE004477; GB:AE004477; GB:AE004497; GB: A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: C83595 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 probable cation efflux system protein PA0397 [imported] - Pseudomonas aeruginosa C;Specites: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83595 FMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILG Conservative 19.3%; 62; Score 372; DB 2; Pred. No. 5.3e-24; Mismatches 109; Length 299; Indels 14; an opportunistic P.; Gaps 86 Hickey, Larbig, <u>ن</u> GSPDB:GN ж., (str н:

286 355

> 193 263 144 203

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A;Cross-references: EMBL:X17537; NID:g4835; PIDN:CAB5654;
C;Genetics:
A;Gene: SGD:ZRC1
A;Gene: SGD:ZRC1
A;Cross-references: SGD:S0004856; MIPS:YMR243c
A;Map position: 13R
C;Function:
A;Description: cadmium resistance; zinc resistance
C;Function:
A;Description: cadmium resistance; zinc resistance
C;Function:
F;9-25/Domain: transmembrane #status predicted <TM1>
F;9-25/Domain: transmembrane #status predicted <TM3>
F;113-129/Domain: transmembrane #status predicted <TM5>
F;240-256/Domain: transmembrane #status predicted <TM5>
F;240-256/Domain: transmembrane #status predicted <TM5>
F;240-256/Domain: transmembrane #status predicted <TM5>
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A; Residues: 1-442 <GEN>
A; Cross-references: EMBL:Z48756; NID:g736304; PIDN:CAA88653.1; PID:g736309; MIPS:YMR243cR; Kamizono, A.; Nishizawa, M.; Teranishi, Y.; Murata, K.; Kimura, A.
Mol. Gen. Genet. 219, 161-167, 1989
A; Title: Identification of a gene conferring resistance to zinc and cadmium ions in the A; Reference number: JQ0349; MUID:90136503; PMID:2693940
A; Accession: JQ0349
A; Molecule type: DNA
A; Residues: 1-413, 'S', 415-416, 'I', 418-442 <KAM>
A; Residues: 1-413, 'S', 415-416, 'I', 418-442 <KAM>
A; Cross-references: EMBL:X17537; NID:g4835; PIDN:CAB56542.1; PID:g5924031
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submitted to the EMBL Data Library, March
A;Reference number: S56053
A;Accession: S56057
A;Molecule type: DNA
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RESULT
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                                                                                                                                                   FH---FHTVTIQIE----DYSEDMK
                                                                                                                                                                                                  SADQIQREILAVPGVIAVHDFHVWNLTESIYIASIHVQI----DCAPDKFMSSAKLIRKI 358
                                                                                                                                                                                                                                                    DFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGK-
                                                                                                                                                                                                                                                                                                                                                   MQSMGVLVAAYILYFKPEYK---YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGV
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Pred. No. 1
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1.6e-22;
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cation efflux system (czcD-like) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998
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E70392
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C; Genetics:
A; Gene: DR1102
A; Map position: 1
C; Superfamily: zinc transporter ZnT-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: A75437
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                   A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70392
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A; Residues: 1-325 <WHI>
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-308 < AQF>
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A;Experimental source: strain R1
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C; Species: Deinococcus radiodurans
                                                                C;Superfamily:
                                                                                                            C; Genetics:
                                                                                                                             A; Experimental source:
                                                                                                                                                 A;Cross-references: GB:AE000721; NID:g2983544; PIDN:AAC07126.1;
                                                                                                                                                                                                               A; Status: preliminary; nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 QEHGHAHGHAHGHDHAAHNHAAGAGERQLTGALVLTGAFLVLEVAYALSSRSLALLSDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIEHVTVQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVER 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSNHHCHAQKGPDSHC--DPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HFHTVTIQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLDALRAELRALPGVQDVHDLHVWSVTGGVVNLTAHLV---SDRAPAELLPAVHEVAHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDLLGSVAVIAGALLIRL-TGWSWVDPLLGAGIGLWVLPRTWSLLKTSVNVLLEGVPEGL
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                                                             zinc transporter ZnT-2
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                                                                                                                             strain VF5
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28.1%;
  18.0%;
27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 351; DB
Pred. No. 3.5e
73; Mismatches
Score
Pred.
                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                  08-May-1998 #text_change 20-Sep-1999
346.5; DB
No. 8e-22;
                                                                                                                                                                                                                   not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
.5e-22;
                      2
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                   Length
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                                                                                                                                                 PID:g2983552; GB:AE00
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T.; Zalewski,
                                                                                                                                                                                                                   not shown
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A; Molecule type: DNA
A; Residues: 1-226; E', 228-332, 'RV', 335-423, 'V', 425-439 <CON>
A; Residues: 1-226; E', 228-332, 'RV', 335-423, 'V', 425-439 <CON>
A; Cross-references: EMBL: M88252; NID: g171262; PIDN: AAA74884.1;
R; Pearson, B. M.; Hernando, Y.; Kalogeropoulos, A.; Schweizer, Machine and Common an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-439 < PEW>
A; Residues: 1-439 < PEW>
A; Cross-references: EMBL: Z75224; NID: g1420693; PIDN: CAA99636.1; PID: e252147; PID: g142069
A; Experimental source: strain S288C
A; Experimental source: strain S288C
R; Pearson, B.M.; Hernando, Y.; Payne, J.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
Yeast 12, 1021-1031, 1996
Yeast 12, 1021-1031, 1996
Yeast 12, 1021-1031, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cobalt accumulation protein COT1 - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein O6131; protein YOR316c

C;Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999

C;Accession: S58327; S31302; S67222; S71996

R;Pearson, B.M.; Hernando, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequencing of a 35.71 kb DNA segment on the right arm A;Reference number: S71986; MUID:97051589; PMID:8896266 A;Accession: S71996
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A;Reference number: State

A;Reference number: State

A;Reference number: State

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                                                                                                   A;Cross-references:
A;Map position: 15R
                                                                                                                                                                                                                        A;Gene:
                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMI
A;Note: the nucleotide
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A; Residues: 1-439 < PEF>
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A; Accession: S58327
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R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A; Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97212
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H97212
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R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gib R;Nolling, J; R;Nolling, J; R;Nolling, J; R;Nolling, G; Omelchenko, M; R;Nolling, G; R;Nolling
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A;Residues: 1-303 <KUR>
A;Residues: 1-303 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80491.1; PID:g15025562; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                       C; Superfamily:
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F;244-265/Domain:
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                                                                                                                                                                                                                                   17.5%;
                                                                                                                                                                                                          86;
                                                                       DISSISKNKLFFVIIFNFIIALAEVIGGSISGSLSLIS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                       Score 336.5; DB 2;
Pred. No. 5.5e-21;
6; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 337;
Pred. No. 7
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.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeng, Q.; Gibson,
                                                                                                                                                                                                          31;
                                                                                                                                                                                                       Gaps
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RESULT 31

$54303

S54303

S10c transport protein ZnT-1 - rat

N;Alternate names: zinc transporter ZnT-1

C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: $54303
R;Palmiter, R.D.; Findley, S.D.
EMBO J. 14, 639-649, 1995
A;Title: Cloning and functional characterization of a mammalian zinc transporte A;Reterence number: $54302; MUID:95188868; PMID:7882967
A;Accession: $54303
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-507 <PAL>
A;Cross-references: EMBL:U17133; NID:9577842; PIDN:AAA79234.1; PID:9577843
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                              356 DYSEDMKD----CQ-ACQ 368
                                                                                                                                  304 MHEAGPCWVLYLDPTLCIIMVCILLYTTYPLLKESALILLQTVPKQIDIKHLVKELRDVE
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                                                                                                                                                                                                                                                                     DQEETNTLVANTSNSNGLKADQAEPEKLRSDDPVDVQVNGNLIQESDSLESEDNRAGQLN
                                                                                                                                                                                                                                                                                                                                        LLVNVLGLCLFHHHSGEGQGAGHGHSHGHGHGHLAKGARKAGRAGGEAGAPPGRAPDQEP
                                                                                                                                                                                                                                                                                                                                                                                                          HATQKNTFGWIRAEVMGALVNAIFLTGLCFAILLEAVERFIE-PHEMQQPLVVLSVGVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYK-----YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVE
                                                                                                                                                                                                    MRGVFLHVLGDALGSVIVVVNALVFYFSWKGCTEDDFCVNPCFPDPCKSSVELMNSTQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                           -ATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSRLQGKFHFHTVTIQIEDYSEDMKDCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTPVNLDMDDVKEQLLKIKEIKGVHHFHIWTLDENNIVLEGHIEIDDILVSETRAISDKI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQ--NTDAQAVLKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIHVIGDFMQSMGVLVA-AYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQALEKLTSLKKINANIVIVVALIGLLGNFLSVIILKKGA-----EKSLNVRSS
FASVGSKSSVVPCELACR
                                                               GVEEVHELHVWQLAGSRIIATAHIKCEDPASYMQVAKT---
                                                                                                                                                                                                                                                                                                                                                                        AVNIIMGLTL--HQS-----GHGHSHG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRNRGRLLCMLLTTMEMVLEVVVSRYTASLAMLSDSFHMLSDVLALVVALVAERFARRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERL--ISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Score 335; DB 2; 24.0%; Pred. No. 1.3e-20; tive 73; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
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                                                                 - IKDVFHNHGIHATTIQPE
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C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: G72363
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84459
                                                                                                                                                                                                                                                                                                                                                                          R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable cation transport protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Evidence for lateral gene transfer between Archaea and A; Reference number: A72200; MUID:99287316; PMID:10360571 A; Accession: G72363
                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-300 <S
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A; Residues: 1-284 < ARN>
                                                                                            C; Superfamily: zinc
                                                                                                                    A; Map position:
                                                                                                                                            A; Gene: At2g04620
                                                                                                                                                                C; Genetics:
                                                                                                                                                                                        A; Cross-references: GB: AE002093;
                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                         Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: D84459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
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th 17.4%; S Similarity 27.3%; P 79; Conservative 76;
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                                                                                            transporter
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28.2%; Pred. No. 7.6e-21;
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                                                                                              ZnT-2
                                                                                                                                                                                        NID: g4895164; PIDN: AAD32753.1;
  Score 334; DB 2;
Pred. No. 8.9e-21;
6; Mismatches 118;
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Gaps

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PCC 7120)

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; Irigu Tabata

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zinc transporter ZnT-1 - mouse
c; Species: Mus musculus (house mouse)
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
C; Accession: S54302
R; Palmiter, R.D.; Findley, S.D.
EMBO J. 14, 639-649, 1995
A; Title: Cloning and functional characterization of a mammalian
A; Reference number: S54302; MUID:95188868; PMID:7882967
A; Accession: S54302
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A;Residues: 1-503 <PAL>
A;Cross-references: EMBL:U17132; NID:g577840; PIDN:AAA79233.1;
C;Genetics:
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        DMKD--
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                                                                              LHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH---FHTVTIQIEDYSE
                                                                                                                     GPCWVLYLDPTLCIIMVCILLYTTYPLLKESALILLQTVPKQIDIKHLVKELRDVDGVEE
                                                                                                                                                                                              FIHVIGDEMQSMGVLVAAYILYEK---
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                                                                                                                                                         ----YKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEA
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A;Title: lowncarrance: 217323; MUID:98162722; PMID:300222.
A;Reference number: 217323; MUID:98162722; PMID:300222.
A;Accession: T43140
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-387 <YOS>
A;Cross-references: EMBL:D89236; NID:91749679; PIDN:BAA13897.1;
                                                                                                                                                                                                                probable heavy metal ion resistance protein - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AG2540
R; Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MOID:21595285; PMID:11759840
A;Accession: AG2540
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A; Residues: 1-304 <KUR>
A; Cross-references: GB:AP003602; PIDN:BAB77253.1;
A; Cross-references: Strain PCC 7120
                                                                                                                                                       R;Yoshioka, S.; Kato, K.;
DNA Res. 4, 363-369, 1997
A;Title: Identification o
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A;Genome: plasmid
C;Superfamily: zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHSHSHGHSHE-PTNY-----NRAFIISVALNTGFVVIEVVYGLAANSLALLADAGH
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                                                                                                                                                                                                                                                                                                                                                                            IEHTTIHIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAAVSLGAVLAG-TATVATGWLWFDPVVSLMIVVVIIVSTWQLFQESLNLVTDAVPAGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                   355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter ZnT-2
                                                                                                                                       of open reading frames in Schizosaccharomyces 323; MUID:98162722; PMID:9501991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%;
25.2%;
                                                                                                                                                                                                Nakai, K.; Okayama, H.; Nojima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 332; DB 2;
Pred. No. 1.3e-20;
1; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g17134695;
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22;

Gaps

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106

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112

226

160

346

219 286

279

GSPDB:GN00181

PID:g1749680

pombe

CDNAS

pomb

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probable zinc/cadmium resistance protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T38252
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21781
A;Reference number: Z21781
A;Accession: T38252
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:Z9859; PIDN:CAB11166.1; GSPDB:GN00066; SPDB:SPAC23C11.14
A;Experimental source: strain 972h-; cosmid c23C11
C;Genetics:
A;Gene: SPDB:SPAC23C11.14
A;Map position: 1
C;Superfamily: zinc transporter ZnT-2
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T38252
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QVADSATESSPLLSYTGNHNGAGTSKPVNNHGSIEQDAPKQTKKRNLNMHGVFLHVLGDA
                                                               GLLSNFVGIFLFHDHGHDHPHTHTAQNYDFPEEDDIESVLPSTIVHRCNTSQQEVSHTHT
                                                                                               VAVNIIMGLTL-HQSGHGHSHG-----
                                                                                                                                                                                                                             QRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFGIYDVTIQPE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGNIGVISAALFIKYTDYSWRFLFDPCISILLTFIILFSAIPLCKSAALILLQVAPQSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVADSATESSPLLSYTGNHNGAGTSKPVNNHGSIEQDAPKQTKKRNLNMHGVFLHVLGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLSNFVGIFLFHDHGHDHPHTHTAQNYDFPEEDDIESVLPSTIVHRCNTSQQEVSHTHT
                                                                                                                                                                                               QTRIILLIGIDVTFFFIEIITGYAIDSLALIADSFHMLNDIVSLLV---ALW-ATRLAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDDVSNLINHLDGVESVHELHIWQLSDVKLIATVHVCVSLPDDKGESYTKLTTDIRNVLQ
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                                                                                                                              TSHEPKYTYGWQRAEILGALSNGVFLIALCMFIFMEAIERFIEPP-SVSNPTLMFFVGSL 121
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88
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                                                                                                                                                                                                                                                            16.3%; Score 314; DB 2; I 23.7%; Pred. No. 6e-19; ative 73; Mismatches 119;
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23.7%; Pred. No. 4.9e-19;
tive 74; Mismatches 118;
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                              ENPSVRAAFIHVIGDF
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A; Molecule type: DNA
A; Residues: 1-316 <PAR>
A; Cross-references: GB:AL139077;
A; Experimental source: serotype C
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cation transport protein Cjl163c [imported] - Campylobacter jejuni (strain C;Species: Campylobacter jejuni (c;Species: Campylobacter jejuni (c;Date: 31-Mar-2000 #text_change 03-Jun-2002 c;Date: 31-Mar-2000 #text_change 03-Jun-2002 c;Accession: E81321 c;Accession: E81321 k; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chi C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Basham, G.; Chi C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Basham, G.; Goldon, G.; Goldon, G.; Chi C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Basham, G.; Goldon, G.; Goldon, G.; Goldon, G.; Chi C.W.; Quail, G.; Goldon, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Basham, G.; Goldon, G.; Go
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C; Superfamily:
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                                                          RLQGKFHFHTVTIQ 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANKSCHHNHEEHSHEHHHSHAD-ARSVDKKILKISLLMTFSMMLVQFIYSILSNSLALL
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                                                                                                                                                                                       PKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVH--IAIAQNTDAQAVLKTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDTLHMFSDVFALALSFLAIIAVEKWQDHQKTFGYFRLEVLVAFINALTIILSALFIIYE 128
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KLLHEFEIGHITIQ
                                                                                                                            P--VDIEKVRQVLLLNPSVDEVVDLHITQITNKMLVASMHLKVRVCNLKEFEKLSQDLSH
                                                                                                                                                                                                                                                                LHMMSDLLGSLAVIIGGIVVYFS-DIVYIDTILAIVLSILLLRWAIILLKQSANVLLESS
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308
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26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 309; DB 2;
Pred. No. 1.3e-18;
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probable cation efflux system protein czcD - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: H71078
R;Kawarzabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida DNA Res. 5, 55-76, 1998

Yamamoto, Kushida, N

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RESULT 39 H71078

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A; Note:
C; Geneti
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A;Accession: H71078
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-295 <KAW>
A;Residues: 1-295 <KAW>
A;Cross references: GB:AP00004; NID:g3236131; PIDN:BAA29990.1; PID:g3257307
A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
D33830
cation efflux system membrane protein czcD - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C;Accession: D33830
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <NIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nies, D.H.; Nies, A.; Chu, L.; Silver, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7351-7355, 1989
A;Title: Expression and nucleotide sequence of a plasmid-determined divalent cation effl A;Reference number: A33830; MUID:90017477; PMID:2678100
A;Accession: D33830
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C;Superfamily: zinc transporter ZnT-2
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:M26073
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                  181 TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 LTVAQPVLSVHIAIAQN--TDAQAVLKTASSRLQGKFHFHTVTIQIE 355
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  123 VAVLGLIINLI-SMRMLSSG-----
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                                                                                       64
                                                                                                                                                                                                    61 SHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFS 120
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                                                                                                                                                                        6 SHDHP--GGNERSLKIALALTGTFLIAEVVGGVMTKSLALISDAAHMLTDTVALAIALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                 LWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGENEIHFECHVETEDMLLSEAQKLIDAIADKLK-KFGITHVTIQLE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPLITVLISLYILHESYGILKESIEVLMEAAP-NLDFQKIKEEIESIPKVRNAHHFHAWR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TMNFGWQRAEILGALVSVLSIWVVTGVLYYLAVERLISGDYEIDGGTMLITSGCAVAVNI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRKMMLSFSLNLGITLAEVIGGIISGSLALLSDSLHNFSDSMGIFASYFAIKIGERKKNE
                                                                                     IAIAKRPADKKRTFGYYRFEILAAAFNALLLFGVAIYILYEAYLRLKSPP-QIESTGMFV
                                                                                                                                                                                                                                                                       67;
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                12.8%; Score 245.5; DB 1; 32.5%; Pred. No. 1.8e-13; itive 44; Mismatches 80;
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----QSSSLNVKGAYLEVWSDLLGSVGVIAGAII 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Qy 241 LYFKPEYKYVDPICTFVFSILVLGTT 266
: | : :| : :| | |
Db 172 IRF-TGWAWYDSAIAVLIGLWYLPRT 196
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Search completed: March 18, 2003, 15:41:28 Job time : 25 secs

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Drosophila melanog

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Title:
Perfect score:
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1923
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                                                                                                                                                      20-SEP-2001; 2001WO-US29218.
                                                                                                                                                                                                                                                                                               Human; transporter protein; zinc transporter; pharmacogenomic analysis; diagnosis; drug screening; gene therapy; kidney; testis; heart; placent small intestine; liver; chromosome 1.
                                                                                                                 20-SEP-2000;
19-OCT-2000;
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Human; transporter and ion channel; TRICH; transport disorder; diabetes mellitus; angina; Alzheimer's disease; neurological; epilepsy; stroke; Huntington's disease; meningitis; muscle; myocarditis; cancer; infectious myositis; arrhythmia; asthma; immunological; gene therapy;

Human transporter and ion channel (TRICH)

(first entry)

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Matches 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease or condition mediated by human transporter protein. The proteins also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, inappropriate or unwanted expression of the protein. The nucleic acids are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention has been found to be expressed in humans in the kidney, testis, heart, placenta, small intestine and liver. The gene has been localised to human chromosome 1. The current sequence represents the human transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human transporter proteins, related to zinc transporter subfamily, useful as model for developing human therapeutic targets serves as target for human therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1(a); Fig 2; 75pp; English.
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                                                                                                                                                                                                                                                      cirrhosis, hepatitis, psoriasis and cancers. TRICH DNA is used gene therapy. TRICH DNA is useful for creating knockin humanisc animals (pigs) or transgenic animals (nice or rats) to model hu disease. The present sequence is human TRICH protein.
                                                                                                                                                                                                                                                                                                                                                      treatment of transport disorder e.g. diabetes mellitus, angina, Alzhelmer's disease; neurological disorder e.g. epilepsy, stroke, Huntington's disease, bacterial and viral meningitis, muscle disorder e.g. myocarditis, infectious myositis, arrhythmias, asthma, immunological disorder e.g. acquired immunodeficiency syndrome (AIDS), allergies, atherosclerosis; and cell proliferative disorders e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of functional TRICH and composition comprising TRICH antagonist is useful for treating a disease or condition associated with TRICH overexpression of TRICH. TRICH sequence is used in the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as an immunogen for preparing antibodies which are useful for diagnosing a condition of disease associated with its expression in a subject, and for detecting and purifying it from a sample. TRICH DNA is useful as probe or a primer for assessing toxicity of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human transporters and ion channels (TRICH) and their corresponding nucleic acid sequences. TRICH is useful for screening an agonist/antagonist that modulates its activity. TRICH is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides of human transporters and ion channels, useful diagnosing, treating or preventing transport, neurological, immunological and cell proliferative disorders -
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useful as an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2000;
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MEAKEKQHLLDARPAIRSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-393948/42.
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372; Conser
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                                                                                                                                                                                                            372
                                                                                                       Conservative
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2000US-241700P.
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000US-234842P
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Ramkumar J,
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Xu Y, Lu
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                                                                                                    Score 1923;
Pred. No. 2.8
); Mismatches
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Thornton M, Gandhi AR;
Raumann BE, Bruns CM, Na
DAM, Ison CH, Griffin JA;
                                                                                                                            DB 23;
.8e-198;
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                                                                                                                                                 Length
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                                                                                                                                 Wei M,
                                                                                                                                                            20-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                         Transporter related protein.
                                                                                                                                                                                 20-SEP-2001; 2001WO-US29218
                                                                                                                                                                                              28-MAR-2002.
                                                                                                                                                                                                          WO200224910-A2.
                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                                            Rat;
                                                                                                                                                                                                                                                                      02-OCT-2002
                                                                                                                                                                                                                                                                                    ABB83085;
                                                                                                                                                                                                                                                                                                ABB83085 standard; Protein; 358
                                                                                                                                               石角
                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                            transporter protein; zinc transporter;
                                                                                                                                                                                                                                                                                                                                                           EALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIEDYSED
                                                                                                                                                                                                                                                                                                                                                                                      SHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFS
                                                                                                                                                                                                                                                                                                                                         MKDCQACQGPSD
                                                                                                                                                                                                                                                                                                                                                                                                                 TSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYI
                                                                                                                                                                                                                                                                                                                                                                                                                              TSGCAVAVNI IMGLTLHQSGHGHSHGTTNQQEENPSVRAAF IHVIGDFMQSMGVLVAAY I
                                                                                                                                                                                                                                                                                                                                 MKDCQACQGPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFS
                                                                                                                     2002-404954/43
                                                                                                                                  Ketchum KA,
                                                                                                                                               PE CORP NY
                                                                                                                                                                                                                                     drug
                                                                                                                                                            2000US-234160P
2000US-0691219
                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                     screening; gene therapy
                                                                                                                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                              372
                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                  Francesco V,
                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                  Beasley
                                                                                                                                                                                                                                           pharmacogenomic
                                                                                                                                                                                                                                            analysis;
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condition mediated by human transporter protein. The proteins also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, inappropriate or unwanted expression of the protein. The nucleic acids are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression

The invention relates to an isolated human transporter protein that related to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease or

is

Disclosure; Page 75; 75pp; English.

Novel human transporter proteins, related subfamily, useful as model for developing serves as target for human therapeutics

to zinc transporte human therapeutic

transporter

targets and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                  Human; NOVX; developmental disorder; endocrine disorder; vascular disorder; infectious disease; anorexia; cancer; stroke; neurodegenerative disorder; Alzheimer's disease; acute brain injury; central nervous system disorder; depression; lung disorder; reproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosic, incharation
 15-SEP-2000;
15-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the gene encoding the transporter protein. The gene of the invention has been found to be expressed in humans in the kidney, testis, heart, placenta, small intestine and liver. The current sequence represents a rat amino acid sequence that is relative to the transporter protein of the invention.
                                                        17-SEP-2001;
                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                       28-MAR-2002
                                                                                                                 WO200224733-A2
                                                                                                                                                                        hepatitis; fertility; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                             30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  ABG60226 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SE ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLHQSGHGHSHG----TINQQEENPSVRAAFIHVIGDFWQSMGVLVAAYILYFKPEYKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVASAICLLEMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLMMSSRPATKTMNF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASRSFFGALWKSEASRI----PPVNLPSVELAVQSNHYCHAQKDSGSHPNSEKQRARRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALHQSGHGHSHGHSHEDSSQQQQNPSVRAAFIHVVGDLLQSVGVLVAAYIIYFKPEYKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVASAICLVFMIGEIIGGYLAQSLAIMTDAAHLLTDFASMLISLFSLWVSSRPATKTMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTVAQPVLSVHIAIAQNVDAQAVLKVARDRLQGKFNFHTMTIQIESYSEDMKSCQECQGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPICTFLFSILVLGTTLTILRDVILVLMEGTPKGVDFTTVKNLLLSVDGVEALHSLHIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                transporter-like
2000US-232675P.
2000US-232676P.
2000US-232679P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                           2001WO-US29115
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.6%;
80.1%;
                                                                                                                                                                        hypertension; arteriosclerosis; ischaemia; Grave's disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                protein NOV2c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1493; DB 23;
Pred. No. 5.8e-152;
5; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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Oy Oy

92

GYLAHSLAVMTDAAHLLIDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSI 151

Matches

176;

Conservative

63;

Mismatches

Indels

9;

Gaps

2

38

PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVG

PRERPE-----ELESGGMYHCHSGSKPTEKGANEYAYAKWELCSASAICFIFMIAEVVG

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The invention relates to an isolated NOVX polypeptide selected from CC NOVIA, NOVIA, NOVIAC, NOVZA, The mature form or variant.

CC Also included are a nucleic acid encoding a NOVX protein or variant.

CC Also included are a nucleic acid encoding a NOVX protein or variant.

CC a vector comprising the nucleic acid, cell comprising the vector;

CC an anti-NOVX antibody; and identifying agents that modulate the comprision of the compri
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-2000;
19-SEP-2000;
19-SEP-2000;
20-SEP-2000;
06-OCT-2000;
                                                                                                                                                                                                                galactossemia and hereditary fructose intolerance), tissue disorders (e.g. wiskott-aldrich syndrome, thrombocytopaenia, night blindness and Pick's disease), disorders linked to abnormal angiogenesis, asthma, azoospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, x-linked severe combined immunodeficiency, seizures migraines, inflammation, autoimmune disorders, disorders affecting sle appetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasi infections, hyper- or hypo-thyroidism, endometriosis, fertility, become recommendation or parasi beamouther anaemia. Werner
                                                                                                                                            syndrome, rheumatoid arthritis, Grave's disease, wound healing, mental retardation, psychotic and neurological disorders and ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumours, lung disorders, haematopoietic disorders, autoimmune diseases and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patturajan M,
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                hypertension,
  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-383182/41.
)B; ABK71914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ; Page 22; 210pp; English
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURAGEN CORP.
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                                                                           369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Syptek KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-233801P
2000US-233960P
2000US-23398BP
2000US-240284P
2000US-240498P
2001US-260973P
2001US-264274P
2001US-274862P
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2000US-233522P.
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2000US-233402P
                                                                                                                       The
                                                                                                                                                                                                arteriosclerosis, ischaemia, haemolytic anaemia,
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her E, Ellerman
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47.48;
51.68;
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Thhson G, Millet I,
                                                                                                                       sequence represents a
Score 911.5;
Pred. No. 2.
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  .8e-89;
                               DB
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                          Length
                                                                                                                            protein
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Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                      seizures
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                                                                                                                                                                                                                                                    parasitic
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19-SEP-2000;
19-SEP-2000;
19-SEP-2000;
20-SEP-2000;
06-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        central nervous system disorder; depression; lung disorder; reproductive disorder; tissue disorder; trombocytopaenia; migraine; angiogenesis; asthma; x-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; inflammation; autoimmune disorder; immune disorder; blood disorder; hepatitis fertility; hypertension; arteriosclarosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing.
                                            Mishra VS, Syptek KA, Taupier RJ, Ve
Tchernev VT, Malyankar UM, Shenoy S,
Patturajan M, Burgess CE, Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular disorder; infectious disease; anorexia; cancer; stroke; neurodegenerative disorder; Alzheimer's disease; acute brain injury;
                                                                                                                                                                                                                                                   15-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                           15-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                               17-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Zinc transporter-like protein NOV2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG60224 standard; Protein; 369
N-PSDB; ABK71912
            WPI; 2002-383182/41
                                                                                              (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                       28-MAR-2002
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                                    Gunther E,
                                                                                                                  2000US-233402P.
2000US-233521P.
2000US-233522P.
2000US-233801P.
2000US-233896P.
2000US-240284P.
2000US-240784P.
2000US-24074P.
2001US-26073P.
2001US-274862P.
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2000US-232679P.
2000US-233382P.
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                                    Ellerman
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                                              Vernet CAM, Colman SD, S, Tchernev VT, Padigaru G, Millet I, Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
                                                         Padigaru
                                                         Gorman
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CC infectious disease, parkinson's disease, Huntington's disease, multiple collections disease, parkinson's disease, Huntington's disease, multiple collections disease, parkinson's disease, Huntington's disease, multiple collections and amyotropic lateral sclerosis), acute brain injury (e.g. cross and amyotropic lateral sclerosis), acute brain injury (e.g. cross acute brain injury) (e.g. cross acute brain injury (e.g. cross acute brain injury) (e.g. cross acute brain injury (e.g. cross acute brain injury (e.g. cross acute brain injury) (e.g. cross acute brain injury (e.g. cross acute brain injury) (e.g. cross acute brain in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated NOVX polypeptide selected from NOV1a, NOV1a, NOV1ac, NOV2a, NOV2c, NOV3a, NOV3b, NOV4a, NOV4b, NOV5a, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant. Also included are a nucleic acid encoding a NOVX protein or variant; a vector comprising the nucleic acid; a cell comprising the vector; an anti-NOVX antibody; and identifying agents that modulate the expression or activity of NOVX. NOVX, the nucleic acid, antibody and modulators are useful in the diagnosis, treatment or prevention of developmental disorders, endocrine disorders, vascular disorders,
                                                                                                            hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked mental retardation, psychotic and neurological disorders and neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 20; 210pp; English
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degeneration. The present

sequence represents a NOVX protein

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Best Local :
329
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                                                                                                                                                                                                                                      92 GHIAGSLAVVTDAAHLLIDLTSFLLSLFSLWLSSKPPSKRLTFGWHRAEILGALLSILCI
                                                                                                                                                                                                                                                                                                                              32 PLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVG
                                                                      DVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQ
                                                                                                                  QANASVRAAFVHALGDLFQSISVLISALIIYFKPEYKIADPICTFIFSILVLASTITILK
                                                                                                                                  WVVTGVLVYLACERLLYPDYQIQATVMIIVSSCAVAANIVLTVVLHQRCLGHNH---KEV
                                                                                                                                                                                               WVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQ
                                                                                                                                                                                                                                                     GYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSI
VVRREIAKALSKSFTMHSLTIQMESPVDQDPDCLFCEDPCD
                          AVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQGPSD 372
                                                        DFSTLLMEGVPKSLNYSGVKELTLAVDGVLSVHSLHIWSLTMNQVILSAHVATAASWDSQ
                                                                                                                                                                                                                                                                                                                                                           al Similarity
176; Conserv
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51.6%;
                                                                                                                                                                                                                                                                                                                                                             62;
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Pred. No. 7.5e-89;
2; Mismatches 94;
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RESULT 6 AAB60094 ID AAB

AAB60094 standard;

Protein;

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Best Local S
Matches 171
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18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer.
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide with a human for the diagnosis, prevention and with the immune, reproductive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn
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                                                                                                                                                                                                                                                51 HHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTD 110
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                                                                                                                                                                                                                          YHCHSGSKPTEKGANEYAYAKWKLCSASAICFIFMIAEVVGGHIAGSLAVVTDAAHLLID
                     TIQIEDYSEDMKDCQACQGPSD
                                                       RDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFHFHTV
                                                                                                 SMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAV
                                                                                                                                 YQIQATYMIIVSSCAVAANIVLTVVLHQRCLGHNH---KEVQANASVRAAFVHALGDLFQ
                                                                                                                                              YEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIGDFMQ
TIQMESPVDQDPDCLFCEDPCD
                                          KELILAVDGVLSVHSLHIWSLTMNQVILSAHVATAASRDSQVVRREIAKALSKSFTMHSL
                                                                                      SISVLISALIIYFKPEYKIADPICTFIFSILVLASTITILKDFSILLMEGVPKSLNYSGV
                                                                                                                                                                              LTSFLLSLFSLWLSSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYPD
                                                                                                                                                                                                    FASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGD 170
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DB; AAF27714.
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171; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                           Page 116-117;
                                                                                                                                                                                                                                                                                                                                        such as cancer.
                                                                                                                                                                                                                                                                                                                  320
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Azimzai
                                                                                                                                                                                                                                                                        Conservative
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99US-0148177.
99US-0149357.
99US-0162287.
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nzai Y,
                                                                                                                                                                                                                                                                                 46.9%;
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Lu DAM,
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                      372
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Pred. No. 2.1
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Au-Young
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Patterson
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This invention relates to the DNA and protein sequences of novel CC isolated 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 85041 CC or 84234 proteins. The method of the invention is useful for treating a CC disorder characterised by aberrant activity of 47476, 67210, 49875, CC 46842, 33201, 83378, 84233, 64708, 85041 or 84234-expressing cell in a CC subject. The protein molecules can act as novel diagnostic targets and CC therapeutic agents for controlling aberrant or deficient signal CC transduction resulting, in e.g., haematopoeitic disorders, including CC blood clotting disorders, autoimmune disorders, or disorders related to abnormal cellular proliferation or CC an inability to clear infections (e.g., viral or bacterial infections), CC as well as disorders related to abnormal cellular proliferation or CC disorders of metabolic imbalance (e.g., disorders of lipopolysaccharide biosynthesis or glycogen synthesis) immunological disorders, cellular CC cardiovascular disorders, neurological disorders, or cellular CC mothility and adhesion disorders disorders, e.g., cancer, cell disorders, viral diseases, neurological disorders (e.g., brain CC disorders, pain or metabolic disorders, liver disorders, kidney CC disorders, protein trafficking disorders and disorders associated with bone metabolism. The sequences of the invention are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2000;
30-NOV-2000;
30-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 8 or 84234 polypeptides, useful as reagents or targets for treating diagnosing pain or metabolic, liver, kidney, or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                    Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disorder; leukaemia; immunological disorder; cardiovascular disorder; neurological disorder; cellular proliferation; red blood cell disorder; viral disease; neurological disorder.
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14-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84233; metal transporter; human; infection; haematopoeitic disorder; blood clotting disorder; cancer;
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DB; ABK88011.
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2000US-248365P.

2000US-248365P.

2000US-250077P.

2000US-250176P.

2000US-250327P.
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Best Local :
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                                                                                                                             07-JUN-2000; 2000US-210329P.
14-NOV-2000; 2000US-248980P.
15-MAY-2001; 2001US-291197P.
Claim 2a; Page 111; 115pp; English
                    Pancreatic tumor polypeptide and prevention and/or treatment of ca
                                                                                    Hirst SK, Harlocker
                                                                                                                                                                          31-MAY-2001; 2001WO-US18003
                                                                                                                                                                                                                    WO200194409-A2
                                                                                                                                                                                                                                                                        Human; pancreatic
                                                                                                                                                                                                                                                                                             Human pancreatic
                                                                                                                                                                                                                                                                                                                                                             AAE17562 standard;
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                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                               13-DEC-2001
                                                                                                                                                                                                                                         Homo sapiens
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                                                      AAD28259
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53.1%;
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                                                                                                                                                                                                                                                                                          full-length protein,
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Pred. No. 2.1e-88;
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                    polynucleotide useful in diagnosis, ancer, especially pancreatic cancer
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Best Local S
Matches 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human pancreatic tumour polypeptides and nucleic acid molecules encoding such polypeptides. The invention also relates to compositions and methods for the diagnosis, prevention and therapy of cancer, particularly pancreatic cancer. Sequences of the invention are used in gene therapy and in vaccines. The present sequence is human pancreatic tumour full-length protein.
New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                          Venter JC,
                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                          2001-656860/75
DB; ABL04427.
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2000US-0614150
                                                                                                                                                                                                                                                                                           (first entry)
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                                                                           PWD,
          detection reagent for detecting for elucidating cell signalling
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Best Local S
Matches 181
central nervous system disorder; depression; lung disorder; reproductive disorder; tissue disorder; thrombocytopaenia; migraine angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disordepatitis; fertility; hypertension; arteriosclerosis; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                neurodegenerative disorder; Alzheimer's disease; acute brain injury;
                                                                                                                                                                                                  vascular disorder;
                                                                                                                                                                                                                            Human; NOVX;
                                                                                                                                                                                                                                                                              Human Zinc transporter-like protein NOV2b.
                                                                                                                                                                                                                                                                                                                                       30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                            ABG60225;
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                                                                                                                                                                                             infectious disease; anorexia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 422
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Pred. No. 1.5e
54; Mismatches
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                                                                                                              migraine;
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06-OCT-2000;
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15-SEP-2000;
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2000US-233402P
2000US-233402P
2000US-233521P
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2000US-23352P
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2000US-23399B
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remer VT, Malyankar Uh Patturajan M, Burgess CE, Stone D, Gunther E, Elle ٧S, V VI, Syptek KA, Ellerman K; Taupier RJ, Ve. UM, Shenoy S, CE, Smithson G, Vernet CAM, Co S, Tchernev VT, G, Millet I, Colman SD, Peyman Padigaru Gorman ۲

N-PSDB; 2002-383182/41. DB; ABK71913.

New cytoplasmic, nuclear, polypeptides, useful for haematopoietic disorders, , membrane bound and secreted NOVX treating cancers and tumours, lung disorders , autoimmune diseases and immune disorders lung disorders,

Claim 1; Page 21; 210pp; English.

migraines, inflammation, autoimmune disorders, disorders affecting sleappetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasi infections, hyper- or hypo-thyroidism, endometriosis, fertility, reproductive disorders, disorders affecting carbohydrate metabolism (e.g. galactosaemia and hereditary fructose intolerance), tissue disorders (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and pick's disease), disorders linked to abnormal anglogenesis, asthma, azoospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, X-linked severe combined immunodeficiency, seizures, infectious disease, anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease, Huntington's disease, multiple sclerosis and amyotropic lateral sclerosis), acute brain injury (e.g. stroke, head injury and cerebral palsy), central nervous system disorders (e.g. depression, epilepsy and schizophrenia), lung disorders, reproductive disorders affecting as the brain disorders. hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-lini mental retardation, psychotic and neurological disorders and neuronal an anti-NOVX antibody; and identifying agents that modulate the expression or activity of NOVX. NOVX, the nucleic acid, antibody and modulators are useful in the diagnosis, treatment or prevention of developmental disorders, endocrine disorders, vascular disorders, NOV1a, NOV1b, NOV1ac, NOV2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV NOV5b, NOV5b or NOV5-NOV9 polypeptides, their mature form or Also included are a nucleic acid encoding a NOVX protein or a vector comprising the nucleic acid; a cell comprising the The invention retardation, psyc...
The present relates to an isolated NOVX polypeptide selected //2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4a, comprising the vector; or variant variant; from, NOV4b, parasitic sleep

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Matches 166;
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                   New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                          Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ
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                                                                                                                                                                                                                                                                                  pharmaceutical.
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                                                                                                                 2001-656860/75
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                                                                                                                                     PWD,
                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No. 2.5
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08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
16-MAR-2001;
16-MAR-2001;
                                                                                                                                                                                                                                                                               1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0840-ABL16175) and the encoded proteins (ABB0737-ABB72072).
                                                  13-OCT-2000;
                                                                                                           WO200230268-A2
                                                                                                                                Mammalia
                                                                                                                                                                    Prostate cancer-associated
                                                                                                                                                                                        15-AUG-2002
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                                                                                                                                                 Prostate cancer;
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2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
2001US-276888P.
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No. 1.6e-77;
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ABG61800-ABG61944 represent prostate cancer-associated proteins.
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Best Local S
Matches 151
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24-APR-2001;
30-APR-2001;
04-MAY-2001;
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|:||: || ||:||:|||::::| ||:|||:|| ||:|| ||:||
|WLSSKSPTKRFTFGFHRLEVLSAMISVLLVYILMGFILYEAVQRTIHMNYEINGDIMLIT 221
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                                                               {\tt DYIKEALMKIED VYSVED LNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTF}
                                                                                                                                                                                                                                                                                                                                     HCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSL 121
                                                                                                                                                                                                                                                                                                                                                                                     EAPERP-VNGAHPTLQADDDSLLDQD---LPLTNSQLSLK----VDSCDNCSKQRE---
   GMYRCTIQLQSYRQEVDRTCANCQSSS
                  HFHTVTIQIEDYSEDM-KDCQACQGPS: | | | :::: | | | | |
                                                                                                                            LVQSVGVLIAAYIIRFKPEYKIADPICTYVFSLLVAFTTFRIIWDTVVIILEGVPSHLNV
                                                                                                                                             151;
                                                                                            TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLQGKF
                                                                                                                                                                                             AAVGVAVNVIMGFLLNQSGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGD
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2001US-0847046.
2001US-288589P.
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The invention relates to prostate specific proteins (PSP) and prostate specific nucleic acids (PSNA). Sequences of the invention are useful for identifying, diagnosing, monitoring, staying, imaging and treating prostate cancer and non-cancerous disease states in prostate. They are also useful for producing engineered prostate tissue for treatment and research. The PSNA sequences are used in gene therapy and for producing transgenic animals and cells. The invention is also used as vaccines. The present sequence is human prostate specific protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              WO200224718-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE24062 standard;
                                                                                                                                               Claim 37; Page 198-199; 210pp; English.
                                                                                                                                                                                   Novel isolated prostate specific polypeptide useful for identifying, diagnosing, monitoring, staging, imaging, and treating prostate can
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                             WPI; 2002-471216/50.
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                                                                                                                                                                          non-cancerous disease states
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prostate cancer; gene therapy; transgenic animal;
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Sequence 438 AA;

Query Match Best Local Matches

Similarity

37.6%;

Score 722.5; DB 2 Pred. No. 8.4e-69;

23;

Conservative

88;

Mismatches

Indels Length

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RESULT 13 AAE24062

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Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 2;
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                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as probes for genetically and physically mapping the s that are a part of, and as markers for traits linked to those s. The present sequence is rice zinc transporter (ZnT-2) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFHTVTIQIEDYSEDM-KDCQACQGPS 371 : | | | | |
GWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGL
                                                                                                                                                                                                        PKMDSHNSAPPQIAEVRMDISSSTSVAAGNKVCRGAACDFSDSSNSSKDARERMASMRKL
                                                                                                                                                                                                                                                              PK------QRQL
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                                                                                                                                                                                                                                                                                                                                                                          RSYTGSLWQEGAGWIPLPRPGLDLQAIELAAQSNHHCHAQKGPDSHCD------
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                                                                                      IIAVILCIIFMAVEVVGGIKANSLAILTDAAHLLSDVAAFAISLFSLWAAGWEATPQQSY
                                                                                                                                               YVASAICLLFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 656.5; DB 2
Pred. No. 1.2e-61;
2; Mismatches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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Query Match Best Local S Matches 142

Local Similarity

Conservative

33.9%;

Score 651.5; Pred. No. 3.9e 71; Mismatches

.9e-61; DB 22; 100;

Indels Length

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Gaps

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RESULT 15
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                                    The invention relates to heavy metal (e.g. arsenite and zinc) transporter polypeptides and polynuclectides. The polypeptides of the invention are useful for producing antibodies that are useful for screening cDNA expression libraries to isolate full length clones of interest. The antibodies are also useful for detecting the polypeptides in situ, in cells or in vitro, in cell extracts. Nucleic acid molecules of the invention are useful for producing transgenic plants with altered tolerance to heavy metals. They are also useful as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those
Sequence
                                                                                                                                                                                             Example 4; Fig
                                                                                                                                                                                                                                    New arsenic transporter polypeptides and polynucleotides, useful for producing transgenic plants with altered level of heavy metal toleran
                                                                                                                                                                                                                                                                                 N-PSDB; AAD16065
                                                                                                                                                                                                                                                                                                                         Allen SM,
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448
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                         sequence is
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                   Protein identification; hybridisation assay; gentermination sequence.
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Local Similarity 37.9%;
nes 134; Conservative 7
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 990S-0121825.
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Pred. No. 5.3e-61;
1; Mismatches 88;
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Best Local Similarity 38.6%;
Matches 132; Conservative
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                    AAG43479 standard; Protein; 344
 AAG43479;
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990S-0139453. 990S-0139454. 990S-0139455. 990S-0139456. 990S-0139457. 990S-0139457. 990S-0139460. 990S-0139460. 990S-0139461. 990S-0139462. 990S-0139463.	99US-0134218 99US-0134211 99US-0134211 99US-0134768 99US-0135124 99US-0135124 99US-0135629 99US-0136021 99US-0136021 99US-0136722 99US-0137722 99US-0137728 99US-0137724 99US-0137724 99US-0138640 99US-0138640 99US-0139119 99US-0139452	990S-0123548 990S-0125788 990S-0126785 990S-0126785 990S-0126785 990S-0128714 990S-0128714 990S-0130077 990S-0130449 990S-0130449 990S-0131449 990S-0131449 990S-0132485 990S-0132485 990S-0132486 990S-0132486 990S-0132486	1000 (first entry) sis thaliana protein fragment SEQ ID NO: 54350. identification; signal transduction pathway; metabolic pathway; attion assay; genetic mapping; gene expression control; promoter; ion sequence. 15.A2. 1000.
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1999; 99US-0118 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119 1999; 99US-0119		1999 1999 1999 1990	1999 1999 1999 1999 1999 1999 1999 1999 1999 1999 1998 1999 1998 1999 1998

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254
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les 132; Conserv
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CTFVFSILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTV
                   TEQLLDKSKTQVAAKEKRKRNINLQGAYLHVLGDSIQSVGVMIGGAIIWYNPEWKIVDLI
                                                      MAVLLGHDHGHSHGHGHGHGHDHHNHSHGVTVTTHHHHHDHEHGHSHGHGEDKHHAHGDV
                                                                       MGLTL----HQSGHGHSHG------TTN-----
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0151066.
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                              -QQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPI
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                                                                                                                                                                  67;
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Pred. No. 2.1e-60;
7; Mismatches 85;
                                                                                                                                                                                  Length 344;
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313
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RESULT 20
AAE09323
ID AAE093
XX AAE09
AC AAE09
AC Soybs
XX Heavy
KW Soybs
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XX Heavy
KW Soybs
XX Glyc:
XX US62:
XX 14-DI
XX 14-DI
XX 14-DI
XX New
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Best Local 9
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                  The invention relates to heavy metal (e.g. arsenite and zinc) transporter polypeptides and polynucleotides. The polypeptides of the invention are useful for producing antibodies that are useful for screening cDNA expression libraries to isolate full length clones of interest. The antibodies are also useful for detecting the polypeptides in situ, in cells or in vitro, in cell extracts. Nucleic acid molecules of the invention are useful for producing transgenic plants with altered tolerance to heavy metals. They are also useful as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to thos genes. The present sequence is soybean zinc transporter (ZnT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New arsenic transporter polypeptides and producing transgenic plants with altered
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig
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N-PSDB; AAD16067.
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                               LVSIQMIWLLAGILVYEAIDRIIAGPKNVDGFLMFLVSAFGLVVNIIMALLLGHDHGHRH
                                                      LVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTL----HQ-
                                                                                                           MIGEVVGGYLAHSLAVMTDAAHLLTDEASMLISLESLWMSSRPATKTMNEGWQRAEILGA 144
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                                                                                              MTVEVVGGIKANSLAILTDAAHLLSDVASFAISLFSLWAAGWEATPRQSYGFFRIEILGA 64
                                                                                                                                                             al Similarity
128; Conserv
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Pred. No. 3.3e
52; Mismatches
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les 81;
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			2 ID NO: 25126. ion pathway; metabolic pathway; ne expression control; promoter;	SHGFTMSTHCDAKHTKDQHHHTHHDENHPKDAHHHTDEDHLHHHA 184 GTTNQQEENPSVRAAFIHVIGDFMQSMGVLVAAYILYFKPBYKYVD 251 ::: :: !: !: ! ! ! ! ! :: :: GTKKKKQWNINVQGAYLHVLGDSIQSUIGGAVLMYNPRMOIVD 244 TLTILRDVILVLMEGTPKGVDFTAVRDLLLSVGVEALHSLHIWAL 311 : : ::
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N-PSDB; ABL09614.
                                                                                                    Venter JC, Adams
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11-JUL-2000;
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les 118; Conservative
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Arabidopsis thaliana

protein fragment SEQ

IJ NO:

pathway; promoter;

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RESULT 2
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                                                                                                                                                   diagnosing disorders
                                                                                                                                                        Isolated 47476, 67210, 49875, or 84234 polypeptides, useful diagnosing pain or metabolic, disorders
                                                                                               Disclosure; Fig
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                                                                                                                                                                  46842, 33201, 83378, 84233, 64708, 85041 as reagents or targets for treating or liver, kidney, or cardiovascular
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This invention relates to the DNA and protein sequences of novel isolated 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, or 84234 proteins. The method of the invention is useful for tree

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
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Best Local S
Matches 110
                                      85041; cation efflux domain; infection; cancer; haematopoeitic disorder; blood clotting disorder; haematopoeitic disorder; leukaemia; immunological disorder; autoimmune disorder; leukaemia; immunological disorder; cellular proliferation; cardiovascular disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Synthetic
                                                                                                                                                                                                                                                                               Human 85041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99931 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHKFGIEHVTVHVEPASEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLIAALLIYFTGYSFKGWKWWYYADPIASILISLIILYTAFRLLKESVLILLEGTPSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WQRAEILGALVSVLSIWVVTGV-LVYLAVERLISGDYEID---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGKFHFHTVTIQIEDYSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DF-TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTD---AQAVLKTASSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110;
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10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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76 ω

Gaps

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62

123 175

GGVALGVALGGTALVVLLGLVVNLALHGYLRRVGKKLKSEHNLNVRAAALHVLGDALSSV GGTMLITSGCAVAVNIIMGLTLHQSGHGHSH--GTTNQQEENPSVRAAFIHVIGDFMQSM HHRAETLAALLNSVFLVIVSFLEILYEAIERLISPDYEIPPDAVLAADIMEPEEPGLFEV

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cc differentiation, e.g., leukaemia. They may also be used to control cc disorders of metabolic imbalance (e.g., disorders of lipopolysaccharide cc biosynthesis or glycogen synthesis) immunological disorders, control cardiovascular disorders, neurological disorders, cell crolliferation and/or differentiation disorders, e.g., cancer, cell controllity and adhesion disorders differentiative disorders, red blood cc cell disorders, viral diseases, neurological disorders, red blood cc disorders, viral diseases, neurological disorders, kidney controlled disorders, pain or metabolic disorders, liver disorders, kidney considers, disorders of the small intestine, disorders of metal in the invention are also useful for screening assays, predictive medicine (e.g., diagnostic assays, controlled trials, and pharmacogenetics); cand methods of treatment (e.g., therapeutic and prophylactic). The cc present sequence represents a predicted consensus sequence motif cc found in the protein of the invention.
                             Query Match
Best Local :
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-2000;
14-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 8 or 84234 polypeptides, useful as reagents or targets for treating diagnosing pain or metabolic, liver, kidney, or cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to the DNA and protein sequences of novel isolated 47476, 67210, 49875, 46842, 33201, 8378, 84233, 64708, 85041 or 84234 proteins. The method of the invention is useful for treating a disorder characterised by aberrant activity of 47476, 67210, 49875, 46842, 33201, 8378, 84233, 64708, 85041 or 84234-expressing cell in a subject. The protein molecules can act as novel diagnostic targets and therapeutic agents for controlling aberrant or deficient signal transfer to the controlling aberrance transfer to the controlling aberrant or deficient signal transfer to the controlling aberrance transfer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transduction resulting, in e.g., haematopoeitic disorders, including blood clotting disorders, autoimmune disorders, or disorders related to an inability to clear infections (e.g., viral or bacterial infections), as well as disorders related to abnormal cellular proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                              Sequence
110;
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                                    Similarity
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                                                                                                                              322 AA;
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2000US-248365P.

2000US-248365P.

2000US-250077P.

2000US-250077P.

2000US-250176P.

2000US-250327P.
Conservative
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                                 24.4%;
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70;
                             Score 469;
Pred. No. 1.
   Mismatches
                                    DB 23;
         105;
                                                                     Length 322;
         Indels
         34;
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RESULT 29
AAU99932
ID AAU99932
XX AAU99932
XX AAU99932
XX AAU9932
XX AAU9
XX AAU8
XX B423
KW B423
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                  This invention relates to the DNA and protein sequences of novel consisted 47476, 67210, 49875, 46842, 33201, 8378, 84233, 64708, 85041 CC isolated 47476, 67210, 49875, 46842, 33201, 8378, 84233, 64708, 85041 CC or 84234 proteins. The method of the invention is useful for treating a CC disorder characterised by aberrant activity of 47476, 67210, 49875, CC 46842, 33201, 83378, 84233, 64708, 85041 or 84234-expressing cell in a CC subject. The protein molecules can act as novel diagnostic targets and CC therapeutic agents for controlling aberrant or deficient signal CC transduction resulting, in e.g., haematopoeitic disorders, including CC blood clotting disorders, autoimmune disorders, or disorders related to CC an inability to clear infections (e.g., viral or bacterial infections), CC differentiation, e.g., leukaemia. They may also be used to control CC disorders of metabolic imbalance (e.g., disorders of lipopolysaccharide CC biosynthesis or glycogen synthesis) immunological disorders, carlot cardiovascular disorders, neurological disorders, or carlot cardiovascular disorders, neurological disorders, or carlot cardiovascular disorders, or carlot cardiovascular disorders, or cardiovascul
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14-NOV-2000;
14-NOV-2000;
30-NOV-2000;
30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or 84234 polypeptides, useful diagnosing pain or metabolic, disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curtis
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; 2000US-248362P.
; 2000US-248365P.
; 2000US-25007P.
; 2000US-250076P.
; 2000US-250327P.
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       differentiation disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucksmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46842, 33201, 83378, 84233, 64708, 6 as reagents or targets for treating liver, kidney, or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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RESULT 30
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Best Local
                                                                                                                                                                                                                                ORFX; human; pharmacogenomics; cancer; hyperproliferative disorder; dysproliferative disorder; neurodegenerative disorder; organ transplant; cardiovascular disease; cytokine; cell proliferation; immunomodulatory; cell differentiation; haematopolesis; tissue growth; thrombolytic; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antificrility; anticonvulsant; vasotropic; antiparkinsonian; dermatological; antirheumatic; antituner; antiulcer; osteopathic; tranquiliser; cerebroprotective; hepatotropic; antiinflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell disorders, viral diseases, neurological disorders (e.g., brain disorders), pain or metabolic disorders, liver disorders, kidney disorders, disorders of the small intestine, disorders of metal ion imbalance, protein trafficking disorders and disorders associated with bone metabolism. The sequences of the invention are also useful for screening assays, predictive medicine (e.g., diagnostic assays, predictive medicine (e.g., diagnostic assays, and methods of treatment (e.g., therapeutic and prophylactic). The present sequence represents a predicted consensus sequence motif
                                                         06-APR-2000;
05-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB53142 standard;
                                                                                                         06-APR-2001;
                                                                                                                                         18-OCT-2001
                                                                                                                                                                      WO200177155-A2
                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB53142;
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                            (CURA-) CURAGEN CORF
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                                                                                                                                                                                                                                                                                                                                                                                             ORF 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
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                                                         2000US-195576P
2001US-0826734
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5; Mismatches
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Pred. No. 6.
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Vernet CAM,

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Leach MD,

Shimkets

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RESULT 31
ABB48454
ID ABB48454
AC ABB486
AC ABB4886
AC ABB488
AC ABB4886

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Best Local
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                                           Dussurget O, Cheto Daniels J, Goebel Dominguez-Bernal G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of human ORFX, where X is any number between 1 and 132. These sequences can be used to diagnose and treat ORFX related disorders, including cancer, hyperproliferative and dysproliferative disorders, neurodegenerative disorders, disorders related to organ transplantation or cardiovascular disorders, disorders related to organ transplantation or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulatory, haematopoiesis regulating, tissue growth, inhib activin, chemotactic or chemokinetic, haemostatic or thrombolytic and or antiinflammatory activities. The present sequence is one or and or antiinflammatory activities.
                            Chakraborty T,
                                                                                                                        Buchrieser C,
                                                                                                                                                                                                                            11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; vitamin Bl2; ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 90; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                           (INSP
                                                                                                                                                                                                                                                                          11-APR-2001;
                                                                                                                                                                                                                                                                                                                             18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                           WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, and may have cell proliferation or differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zerhusen
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cancer, Alzheimer's disease, atherosclerosis, diseases
th liver, comprises polypeptides and polynucleotides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
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84; Conservative
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                       C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux D, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossai Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA.; Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend T, Domann E, Hain T, Berche P, Charbit A, Durant I
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bacterial infection; disease.
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Pred. No. 5.2e
21; Mismatches
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  Del
  Portillo
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5.2e-38;
37;
Charbit A,
o F, Gomez-I
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                         Durant L;
                                                                                                 Dehoux P;
Cossart
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inhibin or
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Matches Query Match Best Local

l Similarity 93; Conser

Conservative

72;

Indels

Gaps

5

Score 414.5; DE Pred. No. 7.4e-3 72; Mismatches 1

DB 127; 23;

Length

303; 17;

21.6%;

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The present invention relates to the genome sequence of Listeria CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of ct it are useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic ct polymorphisms and other genomes. The present sequence is a protein cenceded by the genome sequence of the present invention. Proteins ct expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and cfor biosynthesis and biodegradation, especially biosynthesis of vitamin cc selecting compounds that regulate gene expression and cell replication cand modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and compounds that regulated diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maduenio
Rose M,
                               monocytogenes and related organisms.
Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Claim
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ss H;
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AA;
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                                                                                      n pharmaceutical and prevention of infection
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                                                     part of the printed directly from WIPO
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347
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                                                                                                                                                                                DFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGVD
                                                                                                                                                                                                                                                                                                                                                                                                    AHNHDHAHGHNHNHAHNANKK-----SLFISFILIATFMVVEVIGGIMTNSLALLSDAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                             AQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSLAVMTDAAH
LEHSTIQLE
                                   FHTVTIQIE
                                                                           TEEIKTFFQQQDGVKEVHDLHVWAITSDFNALSAHLTVCEDADRDKILADIEHYLQENFS
                                                                                                                   FTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDAQAVLKTASSRLQGKFH
                                                                                                                                                           DLLGSVGAIIAALLIIFL-GWNIADPIASVIVAALILVSGWRVLKDAIHILMEGKPANVD
                                                                                                                                                                                                                                          FDPPQVIGAGMMTI-SVIGLLINILVAWILMK-----GDTS---ENLNMRSAFLHVLG
                                                                                                                                                                                                                                                                            ISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAAFIHVIG
                                                                                                                                                                                                                                                                                                                        MLSDAVALGLSLAAFKFGEKAASSDKTYGYKRFEILAAFLNGLTLVGISVFIFYEAIGRF
                                                                                                                                                                                                                                                                                                                                                            LLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERL 166
293
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                                                                                                                   346
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RESULT 32
ABP39345
ID ABP39
XX
Staphylococcus epidermidis ORF
                                 24-JUL-2002
                                                             ABP39345
                                                             standard;
                                  (first entry)
                                                             Protein;
                                                             342
                    amino acid
                   sequence SEQ
                     ID NO:4190.
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Staphylococcus antibacterial;

epidermidis; gene therapy.

open

reading

frame;

ORF;

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RESULT 33
ABP40773
ID ABP40
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AC ABP40
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Best Local Similarity
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1997;
08-NOV-1997;
               ABP40773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1998;
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                                        ABP40773 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                             PLPRPGLDLQAIELAAQSNH-HCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVV
                                                                                                                                                                                                                                     QEENPSVRAAFIHVIGDEMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTIL
                                                                                                                                                                                                                                                                                                        IWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQ
                                                                                                                                      Q---AVLKTASSRLQGKFHFHTVTIQIEDYSEDMKDCQACQG
                                                                                                                                                                 KSSLNILMEGTPNDIDLNAVIKAISKDERIQNVHDCHVWTISNDMNALSCHAVVPEYLSV
                                                                                                                                                                                                                       TSHNLNMRGAFLHVLGDLFGSVGAIVAS-LLIWGFNFTIADPIASILVSLIILKSAYGIS
                                                                                                                                                                                                                                                                                                                                                            GGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLS
                                                                                                                                                                                                                                                                                                                                                                                       PFTTPNILVKVEFLMTNHNHQHHHSHAHGHVHTDNKK-----VLMFSFIIISLFMLVEII
                                                                                                            QTCETMLKSIESDLL-QLNIQHMTIQLETPEHKHDESTLCSG
                                                                                                                                                                                          RDVILVLMEGTPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA 330
                                                                                                                                                                                                                                                                              LFIISIIIIIEAIRRFLEPP-EVQSKEMFIISVIGLMVNIIVAILMFKGG------D
                                                                                                                                                                                                                                                                                                                                   GGFLANSLALLSDGFHMLSDAISLGVALIAFIYAEKHATKSKTYGYKRFEILAALFNGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 4190;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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97US-064964P
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                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
                                         359
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 408.5; DB 23;
Pred. No. 4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID 5618; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998;
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 326
                                                        266
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DLLKTQYGLEHVTLQIEN 343
                                                                                                                                                                                                                                                       MTDAAHLLTDFASMLISLFSLWMSSRPATKTMNFGWQRAEILGALVSVLSIWVVTGVLVY 160
                                                                                                                               FIHVIGDFMQSMGVLVAAYILYFKPEYKYVDPICTFVFSILVLGTTLTILRDVILVLMEG
                                                                                                                                                                                                                                                                                    NRRIHAWRRDMENKPDYFHHIEHRKFQSSSKITLWLSLVITMIFTVVEFVGGIVSNSLAL
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DB; ABN93318.
                          SRLOGKFHFHTVTIQIED 356
                                                                                 TPKGVDFTAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQN--TDAQAVLKTAS
                                                                                                              LWHFIGDLLNSLGIIVAFVLIHF-TGWNIVDPIISILISLIILRGGYKIIKNASKVLMER
                                                                                                                                                                                                 LAVERLISGDYEIDGGTMLITSGCAVAVNIIMGLTLHQSGHGHSHGTTNQQEENPSVRAA
                                                                                                                                                                                                                            LSDSFHMLSDVLALGLSMVAIYESSKPPTKNYTYGFLRLEIIVAFLNGLALIVISLGIMY
                                                                                                                                                                     EGIMRIIH-PRPVESGIMILIAFIGLIANIVLTIILMIS-----LKKENNINIQSA
                                                        VPDRYDTDEIMGAMKDVEGVIDIHEFHLWSVTTNQSSLSAHVVLSDDYIKSPYATINKVS
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              site
                                                                                                                                                                                                                                                                                                                                                                                                  359 AA;
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis ORF amino acid sequence
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gene therapy
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97US-064964P
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27.7%;
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Pred. No. 1.5e-32;
9; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frame;
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                                                                                                                                                                                                                                                                                                                                                                      Length 359;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial infection;
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RESULT 34
ABB57822
ID ABB57822
ID ABB57822
AC ABB57
XX ABB57
XX ABB57
XX Drosc
XX Drosc
XX Drosc
XX Pharm
XX Pharm
XX Pharm
XX Pharm
XX Pr 23-MJ
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR04584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment - shows good promotor activity in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pZN10; promotor; yeast; expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promotor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein product of plasmid pZN10 containing a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                   189 NIIMGLTL-HQSG----HGHSHGTTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 ILVLGTTLTILRDVILVLMEGTPKGVDFTAVRDLLL-SVEGVEALHSLHIWALTVAQPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 RQLYVASAICL--LFMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLFSLWMS-SRPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                           S
GNIGVIAAALFIW-KTEYSWRYYSDPIVSLIITIIIFSSALPLSRRASRILLQATPSTI
                                                                                                                                                                                                                                                                                                                                               TKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAV 188
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                                                                                                                                                                                                            SNYVGLFLFHDHGSDSVHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAIS
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                                                                                                       SPGPSGQIGEVLPQSVVNRLSNESQPLLNHDDHDHSHESKKPGHRSLNMHGVFLHVLGDA
                                                                                                                                                                                                                                                                                                                 DAKYTYGWKRAEILGALINAVFLIALCFCIMIEALQRLIE-PQEIQNPRLVLYYGVAGLI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is useful in various foreign gene expressing vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                           -QQEENP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 358; DB 11;
; Pred. No. 1.6e-29;
80; Mismatches 108;
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RESULT 37
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Best Local
                                                                                                                                                                                                                                                                                                                                         This sequence is encoded by the OSR gene from S. cerevisiae strain SD-H. The recombinant yeast containing the OSR DNA sequence was us in the preparation of glutathione by peroxide resistant microbes. Glutathione produced by the recombinants is secreted in to the culture medium and collected. It is useful in drugs and foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of glutathione using peroxidase resistant yeast - useful in the manufacture of drugs and foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-203162/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP08070884-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSR; S. cerevisiae strain DKD-5D-H; glutathione;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast OSR
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                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 6-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR95451;
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                                                                                                                              189 NIIMGLTL-HQSG----HGHSHGTTN----
                                                                                                                                                                                 129 TKTMNFGWQRAEILGALVSVLSIWVVTGVLVYLAVERLISGDYEIDGGTMLITSGCAVAV 188
                                                                                                                                                                                                                                    72 ROLYVASAICL--LEMIGEVVGGYLAHSLAVMTDAAHLLTDFASMLISLESLWMS-SRPA 128
                                                                                                                                                                                                             5 KELRIISLLTLDTVFFLLEITIGYMSHSLALIADSFHMLNDIISLLVALWAVDVAKNRGP
                      MQSMGVLVAAYILYFKPEYK----YVDPICTFVFSILVLGTTLTILRDVILVLMEGTPKGV
                                                                                                      SNYVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAIS
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                                                   SPGPSGQIGEVLPQSVVNRLSNESQPLLNHDDHDHSHESKKPGHRSLNMHGVFLHVLGDA
                                                                                                                                                          DAKYTYGWKRAEILGALINAVFLIALCFSIMIEALQRLIE-PQEIQNPRLVLYVGVAGLI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SADQIQREILAVPGVIAVHDFHVWNLTESIYIASIHVQI----DCAPDKFMSSAKLIRKI 358
                                                                                                                                                                                                                                                                1 Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                    429 AA;
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                Score 357; DB 17;
Pred. No. 2e-29;
80; Mismatches 108;
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                                                                                                                                                                                                                                                               108; Indels 100;
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used
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RESULT 38
AAG91156
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                                                                                    Query Match
Best Local S
Matches 92
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                        sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; organic acid synthesi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression
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                                          DLQAIELAAQSNHHCHAQKGPDSHCDPKKGKAQRQLYVASAICLLFMIGEVVGGYLAHSL
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DB; AAH66375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides useful for detection inappropriately expressed proteins for the screening, and therapeutics -
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                                                                                                            SLYEAGPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQIDIRNLIKELRNV
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Amino acid sequence of a human transporter protein
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